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(54) Title: RECIPROCAL SUBTRACTION DIFFERENTIAL DISPLAY

(57) Abstract

This invention provides a method for identifying differentially expressed nucleic acids between two samples, comprising: a) selecting a first and second nucleic acid sample; b) producing libraries for the first and second nucleic acid sample; c) performing reciprocal subtraction between the libraries to produce two subtracted libraries; d) amplifying the two subtracted libraries; and e) comparing the two amplified subtracted libraries to identify differentially expressed nucleic acids. Also, this invention provides the above-described method, wherein the 3' primer used in the PCR amplification is an oligo dT 3' primer. This invention also provides the above-described methods, wherein the comparing of step e comprises using a gel to separate the nucleic acids from both of the libraries. This invention provides the isolated nucleic acid identified by the above-described methods, wherein the nucleic acid was not previously known to be differentially expressed between the two samples.

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RECIPROCAL SUBTRACTION DIFFERENTIAL DISPLAY

5 This application is a continuation-in-part of U.S. Serial No. 09/197,889, filed November 23, 1998, which is a continuation-in-part of U.S. Serial Application No. 09/185,115, filed November 3, 1998 which is a continuation-in-part of U.S. Serial Application No. 10 09/032,684, filed February 27, 1998. The content of the above identified applications are hereby incorporated into this application by reference.

15 Throughout this application, various references are referred to within parentheses. Disclosures of these publications in their entireties are hereby incorporated by reference into this application to more fully describe the state of the art to which this invention pertains.

20 Background of the Invention

Changes in gene expression are important determinants of normal cellular physiology, including cell cycle regulation, differentiation and development, and they directly contribute to abnormal cellular physiology, including developmental anomalies, aberrant programs of differentiation and cancer (1-4). In these contexts, the identification, cloning and characterization of differentially expressed genes will provide relevant and important insights into the molecular determinants of processes such as growth, development, aging, differentiation and cancer. A number of procedures can be used to identify and clone differentially expressed genes. These include, subtractive hybridization (5-10), differential RNA display (DDRT-PCR) (3,4, 11,12), RNA fingerprinting by arbitrarily primed PCR (RAP-PCR) (13,14), representational difference analysis (RDA) (15), serial analysis of gene expression (SAGE) (16,17), electronic subtraction (18,19) and combinatorial gene matrix analyses (20).

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Since first introduced by Liang and Pardee (11), DDRT-PCR has gained wide popularity in analyzing and cloning differentially expressed genes. In DDRT-PCR, total RNAs or mRNAs from two or more cell types (or cells grown under different conditions, cells representing different stages of development, cells treated with agents modifying cellular physiology, etc.) are reverse-transcribed with two-base-pair anchored oligo dT primers, which divide mRNA populations into 12 cDNA subgroups. Then, each cDNA subgroup is amplified by PCR with one of 20 arbitrary 10-mer 5' primers and a 3' anchored primer and the PCR-amplified cDNA fragments are resolved in DNA sequencing gels. The combinations of primers are designed not only to yield a detectable size and number of bands, but also to display nearly the complete repertoire of mRNA species.

DDRT-PCR is a powerful methodology in which a vast number of mRNA species (>20,000, if no redundancy occurs) can be analyzed with only a small quantity of RNA (about 5 µg) (11). DDRT-PCR is often the method of choice when the RNA source is limiting, such as tissue biopsies. A direct advantage of DDRT-PCR is the ability to identify and isolate both up- and down-regulated differentially expressed genes in the same reaction. Furthermore, the DDRT-PCR technique permits the display of multiple samples in the same gel, which is useful in defining specific diagnostic alterations in RNA species and for temporally analyzing gene expression changes. However, the DDRT-PCR technique is not problem free. Difficulties encountered when using standard DDRT-PCR include, a high incidence of false positives and redundant gene identification, poor reproducibility, biased gene display and lack of functional information about the cloned cDNA. Furthermore, poor separation can mask differentially expressed genes of low abundance under the intense signals generated by highly expressed genes. The

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generation of false positives and redundancy can be highly problematic, resulting in an inordinate expenditure of resources to confirm appropriate differential expression and uniqueness of the isolated 5 cDNAs. The cDNAs must be isolated from the gels in pure form (contamination of bands with multiple sequences complicates clone identification), reamplified, placed in an appropriate cloning vector, analyzed for authentic differential expression and finally sequenced. These 10 limitations of the standard DDRT-PCR approaches emphasize the need for improvements in this procedure to more efficiently and selectively identify differentially expressed genes.

15 A number of modifications and improvements of the DDRT-PCR approach have been described (21-23). Single anchor or degenerate two-base anchor oligo dT primers can be used to streamline the massive numbers of reverse transcription and PCR reactions required for validation 20 of cDNAs as well as to reduce false positives (24,25). Reproducibility can be improved by lengthening the arbitrary 5' primers to accommodate a convenient restriction site followed by two cycles of PCR with successive low- and high-stringency annealing 25 temperatures (25,26). DDRT-PCR with inosine-containing 5' arbitrary primers can also increase reproducibility of this approach (27). However, since these modifications have only been analyzed using a subset of primers, further studies are necessary to validate these 30 modifications of DDRT-PCR with additional primers and in several model systems.

In addition to genomic DNA contamination, mispriming, PCR 35 artifacts, the high incidence of false positives and redundancy is also ascribed to poor separation between bands and the complexity of the templates amplified (28). Furthermore, poor separation can mask differentially

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expressed genes of low abundance under the intense signals generated by highly expressed genes. By enriching for unique cDNAs and removing common ones, it should in principle be possible to enrich for low abundant gene products and significantly decrease the complexity of amplified sequences. In addition, the sequence bias of DDRT-PCR should also be reduced by decreasing template complexity. These assumptions serve as the basis for the development of reciprocal subtraction differential RNA display (RSDD).

Subtractive hybridization, in which hybridization between tester and driver is followed by selective removal of common gene products, enriches for unique gene products in the tester cDNA population and reduces the abundance of common cDNAs (9). A subtracted cDNA library can be analyzed to identify and clone differentially expressed genes by randomly picking colonies or by differential screening (29-31). Although subtractive hybridization has been successfully used to clone a number of differentially expressed genes (5-7,10), this approach is both labor-intensive and does not result in isolation of the full spectrum of genes displaying altered expression (9,18).

In principle, DDRT-PCR performed with subtracted RNA or cDNA samples represents a powerful strategy to clone up and down-regulated gene products. This approach should result in the enrichment of unique sequences and a reduction or elimination of common sequences. This scheme should also result in a consistent reduction in band complexity on a display gel, thereby permitting a clearer separation of cDNAs resulting in fewer false positive reactions. Additionally, it should be possible to use fewer primer sets for reverse transcription and PCR reactions to analyze the complete spectrum of differentially expressed genes. Of particular importance

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for gene identification and isolation, rare gene products that are masked by strong common gene products should be displayed by using subtraction hybridization in combination with DDRT-PCR. In addition, the DDRT-PCR approach with subtractive libraries could also prove valuable for efficiently screening subtracted cDNA libraries for differentially expressed genes. However, even though subtraction hybridization plus DDRT-PCR appears attractive for the reasons indicated above, a previous attempt to use this approach has proven of only marginal success in consistently reducing the complexity of the signals generated, compared with the standard DDRT-PCR scheme (32).

We presently describe a reciprocal subtraction differential RNA display (RSDD) approach that efficiently and consistently reduces the complexity of DDRT-PCR and results in the identification and cloning of genes displaying anticipated differential expression.

20

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Summary of the Invention

This invention provides a method for identifying differentially expressed nucleic acids between two samples, comprising: (a) selecting a first and second 5 nucleic acid sample, wherein the nucleic acid samples contain a repertoire of nucleic acids; (b) performing reciprocal subtraction between the nucleic acid samples to produce two subtracted nucleic acid samples; (c) amplifying the two subtracted nucleic acid samples; and 10 (d) comparing the two subtracted nucleic acid samples to identify differentially expressed nucleic acids.

This invention also provides a method for identifying differentially expressed nucleic acids between two 15 samples, comprising: (a) selecting a first and second nucleic acid sample, wherein the nucleic acid samples contain a repertoire of nucleic acids; (b) amplifying the two nucleic acid samples; (c) performing reciprocal subtraction between the amplified nucleic acid samples to 20 produce two subtracted nucleic acid samples; and (d) comparing the two subtracted nucleic acid samples to identify differentially expressed nucleic acids.

This invention further provides the above-described 25 methods, wherein the first and second nucleic acid samples are obtained from cells in different developmental stages.

This invention further provides the above-described 30 methods, wherein the first and second nucleic acid samples are obtained from cells from different tissue types.

Also, this invention provides the above-described 35 methods, wherein the 3' primer used in the PCR amplification is an oligo dT 3' primer.

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In addition, this invention provides the above-described methods, wherein the 3' primer used in the PCR amplification is a single anchor oligo dT 3' primer.

5 This invention also provides the above-described methods, wherein the comparing of step (e) comprises using a gel to separate the nucleic acids from both of the libraries.

This invention provides the isolated nucleic acid
10 identified by the the above-described methods, wherein the nucleic acid was not previously known to be differentially expressed between the two samples.

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Brief Description of the Figures

Figure 1

Identification of differentially expressed sequence tags
5 using reciprocal subtraction differential RNA display
(RSDD). Left panel: differential RNA display pattern of
conventional DDRT-PCR with RNA from E11 (C) and E11-NMT
(T) cells and an RSDD analysis of reciprocally subtracted
E11 minus E11-NMT (C/T) and E11-NMT minus E11 (T/C) cDNA
10 libraries. Right panel: representative RSDD patterns
using different sets of primers.

Figure 2

Reverse Northern analysis of differentially expressed
15 sequence tags identified by reciprocal subtraction
differential RNA display (RSDD). Differentially expressed
sequence tags obtained from RSDD were dot-blotted onto
Nylon membranes and probed with ³²P-cDNA reverse
transcribed from RNA samples of E11 and E11-NMT cells.
20

Figure 3A

Differential expression of representative progression
elevated genes (PEGen) and progression suppressed genes
(PSGen) identified by reciprocal subtraction differential
25 RNA display (RSDD) and reverse Northern blotting.
Northern blots of E11 and E11-NMT RNA samples were probed
with radiolabeled (³²P) expressed sequence tags identified
by RSDD and reverse Northern blotting.

Figure 3B

Differential expression of representative progression
elevated genes (PEGen) and progression suppressed genes
(PSGen) identified by reciprocal subtraction differential
RNA display (RSDD) and reverse Northern blotting.
35

Figure 4

Differential expression of representative progression

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elevated genes (PEGen) and progression suppressed genes (PSGen) identified by reciprocal subtraction differential RNA display (RSDD) and reverse Northern blotting. Northern blots of cells displaying various stages of transformation progression were probed with radiolabeled (³²P) expressed sequence tags identified by RSDD and reverse Northern blotting. The cell types used include, 5 Unprogressed E11 (-), CREFxE11-NMT F1 (-) and CREFxE11-NMT F2 (-) somatic cell hybrids, E11xE11-NMT A6 10 (-) somatic cell hybrid, E11xE11-NMT 3b (-) somatic cell hybrid, and E11-NMT Aza B1 (-) and E11-NMT Aza C1 (-) 5-azacytidine treated E11-NMT clones; and Progressed 15 E11-NMT (+), CREFxE11-NMT R1 (+) and CREFxE11-NMT R2 (+) somatic cell hybrids, E11xE11-NMT A6TD (+) nude mouse tumor derived somatic cell hybrid, E11xE11-NMT IIa (+), E11-Ras R12 (+) a Ha-ras transformed E11 clone and E11-HPV E6/E7 (+) an E11 clone transformed by the E6 and 20 E7 region of HPV-18.

20 Figure 5

cDNA fragment of PEGen 7 - 90% Homology to Human HPV16 E1BP. (Sequence ID No. 1)

25 Figure 6

cDNA fragment of PEGen 8 - Rat phosphofructose kinase C. (Sequence ID No. 2)

30 Figure 7

First (Sequence ID No. 3) and second (Sequence ID No. 4) cDNA fragments of PEGen 13.

Figure 8

cDNA fragment of PEGen 14. (Sequence ID No. 5)

35 Figure 9

cDNA fragment of PEGen 15. (Sequence ID No. 6)

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Figure 10

cDNA fragment of PEGen 21 which has 94% homology to mouse FIN 14. (Sequence ID No. 7)

5

Figure 11

cDNA fragment of PEGen 24. (Sequence ID No. 8)

Figure 12

10 cDNA fragment of PEGen 26 - Rat poly ADP-ribose polymerase. (Sequence ID No. 9)

Figure 13

cDNA fragment of PEGen 28. (Sequence ID No. 10)

15

Figure 14

cDNA fragment of PEGen 42. (Sequence ID No. 11)

Figure 15

cDNA fragment of PEGen 43. (Sequence ID No. 12)

20

Figure 16

cDNA fragment of PEGen 44. (Sequence ID No. 13)

Figure 17

25

cDNA fragment of PEGen 48. (Sequence ID No. 14)

Figure 18

30 cDNA fragment of PSGen 1 which has 80% homology to *B. taurus supervillin*. (Sequence ID No. 15)

35

Figure 19

cDNA fragment of PSGen 2 which has 91% homology to human HTLV-1 Tax interacting protein. (Sequence ID No. 16)

35

Figure 20

cDNA fragment of PSGen 4 - Rat proteasome activator. (Sequence ID No. 17)

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Figure 21

cDNA fragment of PSGen 10 - Rat Ferritin Heavy Chain.
(Sequence ID No. 18)

5 Figure 22

cDNA fragment of PSGen 12. (Sequence ID No. 19)

Figure 23

cDNA fragment of PSGen 13. (Sequence ID No. 20)

10

Figure 24

cDNA fragment of PSGen 23. (Sequence ID No. 21)

Figure 25

15 cDNA fragment of PSGen 24. (Sequence ID No. 22)

Figure 26

cDNA fragment of PSGen 25. (Sequence ID No. 23)

20 Figure 27

cDNA fragment of PSGen 26.

Figure 28

cDNA fragment of PSGen 27.

25

Figure 29

cDNA fragment of PSGen 28.

Figure 30

30 cDNA fragment of PSGen 29.

Figure 31

cDNA fragment of PEGen 32.

35

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Figure 32

Schematic outline of the reciprocal differential RNA display (RSDD) protocol. This scheme incorporates three steps, reciprocal subtraction of cDNA libraries, differential display of *in vivo* excised cDNAs and expression analysis by reverse Northern and standard Northern blotting. For the present application of RSDD, reciprocal subtraction hybridization was performed using libraries constructed from E11 and E11-NMT cells, i.e., E11 minus E11-NMT and E11-NMT minus E11. Differentially expressed cDNAs identified on gels using differential RNA were isolated, reamplified and analyzed for expression by reverse Northern blotting. To confirm differential expression cDNAs were analyzed using Northern blotting.

Figure 33

Differential expression of representative progression elevated (PEGen) and progression suppressed genes (PSGen) identified by RSDD and reverse Northern blotting.

20 Northern blots of E11 and E11-NMT RNA samples were probed with radiolabeled (³²P) expressed sequence tags identified by RSDD and reverse Northern blotting. Equal loading of E11 and E11-NMT RNA is demonstrated by ethidium bromide (EtBr) Staining .

Figure 34

Differential expression of representative PEGen and PSGen genes identified by RSDD and reverse Northern blotting in a large panel of rodent cells displaying differences in transformation progression. Northern blots of cells displaying various stages of transformation progression were probed with radiolabeled (³²P) expressed sequence tags identified by RSDD and reverse Northern blotting. The cell types used include: Unprogressed E11 (-), CREF X E11-NMT F1 (-) and CREF X E11-NMT F2 (-) somatic cell hybrids, E11 X E11-NMT A6 (-) somatic cell hybrid, E11 X E11-NMT 3b (-) somatic cell hybrid, and E11-NMT AZA B1

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(-) and E11-NMT AZA C1 (-) 5-azacytidine-treated E11-NMT clones; and Progressed E11-NMT (+), CREF X E11-NMT R1 (+) and CREF X E11-NMT R2 (+) somatic cell hybrids, E11 X E11-NMT A6TD (+) nude mouse tumor derived somatic cell hybrid, E11 X E11-NMT IIa (+), E11-Ras R12 (+) and E11-HPV E6/E7 (+) an E11 clone transformed by the E6 and E7 region of HPV-18. Equal loading of RNAs is demonstrated by ethidium bromide (EtBr) staining.

10 Figure 35 A
PSGen 12 cDNA Sequence and PSGen 12 Protein Sequence

Figure 35 B
PSGen 13 cDNA Sequence and PSGen 13 Protein Sequence

15 Figure 35 C
PEGen 28 cDNA Sequence and PEGen 28 Protein Sequence

20 Figure 35D
PEGen 32 cDNA Sequence and PEGen 32 Protein Sequence

Figure 35 E
PEGen 42 cDNA Sequence and PEGen 42 Protein Sequence

25 Figure 35 F
PEGen 45 cDNA Sequence

30 Figure 35 G-1 and Figure 35 G-2
PEGen 50 cDNA Sequence which are different parts of the gene.

Figure 36
PSGen 27 - Novel

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Detailed Description of the Invention

This invention provides a method for identifying differentially expressed nucleic acids between two samples, comprising: (a) selecting a first and second 5 nucleic acid sample, wherein the nucleic acid samples contain a repertoire of nucleic acids; (b) performing reciprocal subtraction between the nucleic acid samples to produce two subtracted nucleic acid samples; (c) amplifying the two subtracted nucleic acid samples; and 10 (d) comparing the two subtracted nucleic acid samples to identify differentially expressed nucleic acids.

In an embodiment, the nucleic acid samples are mRNA or derived from mRNA. In another embodiment, the nucleic 15 acid samples are total RNA. In another embodiment, the nucleic acid samples are cDNA. In another embodiment, the nucleic acid samples are a nucleic acid library.

20 In an embodiment, differentially expressed nucleic acids are expressed at different levels. In a further embodiment, one of the nucleic acids is not expressed. In a different embodiment, one of the nucleic acids is expressed in truncated form.

25 As used herein, reciprocal subtraction includes using nucleic acid sample A to subtract common nucleic acids from nucleic acid sample B (based on hybridization) and also using nucleic acid sample B to subtract common nucleic acids from nucleic sample A. In an embodiment, 30 the complement of nucleic acid sample A is used to subtract nucleic acids from nucleic acid sample B and the complement of nucleic acid sample B is used to subtract nucleic acids from nucleic acid sample A. In a further embodiment, the RNA of nucleic acid sample A is used to subtract nucleic acids from nucleic acid sample B and the RNA of nucleic acid sample B is used to subtract nucleic acids from nucleic acid sample A. In yet another 35

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embodiment, the cDNA of nucleic acid sample A is used to subtract nucleic acids from nucleic acid sample B and the cDNA of nucleic acid sample B is used to subtract nucleic acids from nucleic acid sample A.

5

As used herein, methods of amplification include PCR and rolling circle replication.

A basic description of nucleic acid amplification is described in Mullis, U.S. Patent No. 4,683,202, which is incorporated herein by reference. The amplification reaction uses a template nucleic acid contained in a sample, two primer sequences and inducing agents. The extension product of one primer when hybridized to the second primer becomes a template for the production of a complementary extension product and vice versa, and the process is repeated as often as is necessary to produce a detectable amount of the sequence.

20 The inducing agent may be any compound or system which
will function to accomplish the synthesis of primer
extension products, including enzymes. Suitable enzymes
for this purpose include, for example, *E.coli* DNA
polymerase I, thermostable *Taq* DNA polymerase, Klenow
fragment of *E.coli* DNA polymerase I, T4 DNA polymerase,
other available DNA polymerases, reverse transcriptase
and other enzymes which will facilitate combination of
the nucleotides in the proper manner to form
amplification products. The oligonucleotide primers can
30 be synthesized by automated instruments sold by a variety
of manufacturers or can be commercially prepared based
upon the nucleic acid sequence of this invention.

This invention also provides a method for identifying differentially expressed nucleic acids between two samples, comprising: a) selecting a first and second nucleic acid sample; b) producing libraries for the first

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and second nucleic acid sample; c) amplifying the two libraries; d) performing reciprocal subtraction between the amplified libraries to produce two subtracted libraries; and e) comparing the two subtracted libraries 5 to identify differentially expressed nucleic acids.

This invention also provides a method for identifying differentially expressed nucleic acids between two samples, comprising: (a) selecting a first and second 10 nucleic acid sample, wherein the nucleic acid samples contain a repertoire of nucleic acids; (b) amplifying the two nucleic acid samples; (c) performing reciprocal subtraction between the amplified nucleic acid samples to produce two subtracted nucleic acid samples; and (d) 15 comparing the two subtracted nucleic acid samples to identify differentially expressed nucleic acids.

This invention also provides the above-described methods, 20 wherein the two subtracted nucleic acid samples from step c are amplified prior to the comparing of step d.

This invention also provides the above-described methods, 25 wherein each of the nucleic acid samples comprises a library of nucleic acids.

This invention also provides the above-described methods, 30 wherein the nucleic acid samples are obtained from total cellular RNA purified by hybridization with oligo (dT).

This invention also provides the above-described methods, 35 wherein the nucleic acid samples are obtained from total RNA from E11 and E11-NMT cells.

E11 is an adenovirus-transformed rat embryo cell line 35 that acquires an aggressive oncogenic progression phenotype when injected into athymic nude mice and reisolated in cell culture (E11-NMT).

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This invention further provides the above-described methods, wherein the first and second nucleic acid samples are obtained from cells in different developmental stages.

5

This invention further provides the above-described methods, wherein the first and second nucleic acid samples are obtained from cells from different tissue types.

10

This invention further provides the above-described methods, wherein the first and second nucleic acid samples are obtained from cells that differ in their exposure to external factors or in their gene expression.

15

In an embodiment, cells that differ in their exposure to external factors or in their gene expression includes any cells that may have different levels of gene expression, wherein some genes may not be expressed at all. In another embodiment, cells that differ in their exposure to external factors or in their gene expression includes any cells that are likely to have different levels of gene expression, wherein some genes may not be expressed at all. In still another embodiment, cells that differ in their exposure to external factors or in their gene expression includes any cell that has a phenotypically recognizable difference.

30

A short list of examples of cells that differ in their exposure to external factors or in their gene expression includes: cancerous versus normal cells, advanced cancer progression cells versus earlier cancer stage cells, diseased cells versus nondiseased cells, infected cells versus noninfected cells, later developmental stage cells versus earlier developmental stage cells, cells after DNA damage versus cells before DNA damage, senescent cells versus younger cells, cells induced by growth factors

35

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versus cells not induced by growth factors, cells in the process of neurodegeneration versus normal cells, and cells exposed to a chemotherapeutic agent versus normal cells.

5

As used herein, different tissues types include but are not limited to tissues containing: cells grown under or exposed to different conditions, cells in different stages of development, cells treated with agents 10 modifying cellular physiology, and cells having different functions.

In an embodiment, cells at different stages of development are cells taken or analyzed at times 15 differing by one or more hours in the development of the cell or organism.

Further, this invention provides the above-described 20 methods, wherein the amplifying of step (d) comprises PCR amplification.

Also, this invention provides the above-described 25 methods, wherein the 3' primer used in the PCR amplification is an oligo dT 3' primer. A few examples of oligo dT primers are T₁₃, T₁₃A, and T₁₃GA.

In addition, this invention provides the above-described 30 methods, wherein the 3' primer used in the PCR amplification is a single anchor oligo dT 3' primer. Oligo dT 3' primers include T₁₃A, T₁₃C, and T₁₃G.

This invention provides the above-described methods, 35 wherein the PCR amplification uses a set of random primers.

This invention provides the above-described methods, wherein the 5' primer is an arbitrary primer.

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This invention also provides the above-described methods, wherein the comparing of step (e) comprises using a gel to separate the nucleic acids from both of the subtracted libraries.

5

In an embodiment, the gel is a polyacrylamide gel. In another embodiment, the gel is an agarose gel.

10 This invention further provides the above-described methods, further comprising PCR amplifying the first and second nucleic acid samples.

15 This invention also provides the above-described methods, further comprising reamplifying differentially expressed bands.

This invention also provides the above-described methods, further comprising reamplifying differentially expressed nucleic acid.

20

In one method of reamplifying differentially expressed bands, differentially amplified bands from plasmids of each subtracted library were marked with an 18G needle through the film and cut out with a razor. The cut out differentially expressed bands can be reamplified (i.e. by PCR) and examined by reverse Northern and Northern blot analyses.

30

In addition, this invention provides the above-described methods, wherein the comparing of step (e) comprises comparing the band intensities of the two amplified differentially expressed nucleic acids.

35

In addition, this invention provides the above-described methods, wherein the nucleic acid samples are mRNA or cDNA derived from mRNA.

-20-

In addition, this invention provides the above-described methods, wherein the comparing of step (e) comprises comparing the quantities of the two amplified differentially expressed nucleic acids.

5

This invention further provides the above-described methods, wherein the differences in band intensity between the two subtracted libraries are electronically quantified.

10

This invention further provides the above-described methods, wherein the differences in the quantities of nucleic acid between the two subtracted libraries are electronically quantified.

15

In one embodiment, electronic quantification involves using a scanner to detect the bands. In a further embodiment, computer software, such as Corel Draw, can be used to determine the pixel intensity of the scanned image, thereby quantifying the band intensity.

20
25
Also, this invention provides the above-described methods, wherein the libraries of step (b) are constructed with λ -ZAP cDNA library kits. One skilled in the art would recognize that any cDNA library would be suitable.

30
This invention provides the isolated nucleic acid identified by the the above-described methods, wherein the nucleic acid was not previously known.

This invention also provides the above-described isolated nucleic acid, wherein the isolated nucleic acid is the nucleic acid designated PSGen 12 (AI 144569).

35

In addition, this invention provides the above-described isolated nucleic acid, wherein the isolated nucleic acid

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is the nucleic acid designated PSGen 13 (Accession No. AI 144570).

5 This invention provides the above-described isolated nucleic acid, wherein the isolated nucleic acid is the nucleic acid designated PSGen 23.

10 This invention provides the above-described isolated nucleic acid, wherein the isolated nucleic acid is the nucleic acid designated PSGen 24.

This invention provides the above-described isolated nucleic acid, wherein the isolated nucleic acid is the nucleic acid designated PSGen 25.

15 This invention provides the above-described isolated nucleic acid, wherein the isolated nucleic acid is the nucleic acid designated PSGen 26 (Accession No. AI 144571).

20 This invention also provides the above-described isolated nucleic acid, wherein the isolated nucleic acid is the nucleic acid designated PSGen 27 (Accession No. AI 144572).

25 This invention provides the above-described isolated nucleic acid, wherein the isolated nucleic acid is the nucleic acid designated PSGen 28 (AI 144573).

30 This invention provides the above-described isolated nucleic acid, wherein the isolated nucleic acid is the nucleic acid designated PSGen 29 (AI 144574).

35 This invention provides the above-described isolated nucleic acid, wherein the isolated nucleic acid is the nucleic acid designated PEGen 13 (AI 144564).

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This invention provides the above-described isolated nucleic acid, wherein the isolated nucleic acid is the nucleic acid designated PEGen 14 (AI 144565).

5 This invention provides the above-described isolated nucleic acid, wherein the isolated nucleic acid is the nucleic acid designated PEGen 15.

10 This invention provides the above-described isolated nucleic acid, wherein the isolated nucleic acid is the nucleic acid designated PEGen 24 (Accession No. AI 144566).

15 This invention provides the above-described isolated nucleic acid, wherein the isolated nucleic acid is the nucleic acid designated PEGen 28 (AI 144567).

20 This invention provides the above-described isolated nucleic acid, wherein the isolated nucleic acid is the nucleic acid designated PEGen 32 (AI 144568).

25 This invention provides the above-described isolated nucleic acid, wherein the isolated nucleic acid is the nucleic acid designated PEGen 42.

30 This invention provides the above-described isolated nucleic acid, wherein the isolated nucleic acid is the nucleic acid designated PEGen 43.

35 This invention provides the above-described isolated nucleic acid, wherein the isolated nucleic acid is the nucleic acid designated PEGen 44.

40 This invention provides the above-described isolated nucleic acid, wherein the isolated nucleic acid is the nucleic acid designated PEGen 48.

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This invention further provides a previously unknown isolated nucleic acid molecule identified by the above-described methods which comprises (a) one of the nucleic acid sequences as set forth in Figure 35; (b) a sequence being degenerated to a sequence of (a) as a result of the genetic code; (c) a sequence encoding one of the amino acid sequences as set forth in Figure 35. (d) a sequence of at least 12 nucleotides capable of specifically hybridizing to the sequence of (a), (b) or (c).

Finally, this invention provides a purified polypeptide comprising one of the amino acid sequence as set forth in Figure 35.

The sequences of the cDNA of PSGen 12, PSGen 13, PSGen 15
26, PSGen 27, PSGen 28, PSGen 29, PEGen 13, PEGen 14,
PEGen 24, PEGen 28, and PEGen 32 were submitted to
GenBank and assigned with accession numbers AI 144569, AI
144570, AI 144571, AI 144572, AI 144573, AI 144574, AI
144564, AI 144565, AI 144566, AI 144567 and AI 144568
20 respectively.

This invention will be better understood from the Experimental Details which follow. However, one skilled 25 in the art will readily appreciate that the specific methods and results discussed are merely illustrative of the invention as described more fully in the claims which follow thereafter.

30 Experimental Details

We presently describe a reciprocal subtraction differential RNA display (RSDD) approach that efficiently and consistently reduces the complexity of DDRT-PCR and results in the identification and cloning of genes 35 displaying anticipated differential expression. Proof of principle for the RSDD approach has come from its application for the identification of genes

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differentially expressed during cancer progression. RSDD has resulted in the identification and cloning of genes displaying elevated expression in progressed tumor cells (PEGen) and reduced expression in progressed tumor cells (PSGen). The model used for RSDD was an adenovirus-transformed rat embryo cell line, E11, that acquires an aggressive oncogenic progression phenotype when injected into athymic nude mice and reisolated in cell culture (E11-NMT) (10,33,34). Injection of E11 cells into nude mice results in tumors in 100% of animals with a tumor latency time of approximately 35 to 40 days, whereas E11-NMT cells form tumors in 100% of nude mice with a tumor latency time of 15 to 20 days (10,34,35). Additionally, E11 cells form colonies in agar with an efficiency of ~3%, whereas E11-NMT display an agar cloning efficiency of >30% (10,33,34). The increased tumorigenicity and enhanced anchorage independence phenotypes are key indicators of tumor progression in the E11/E11-NMT model system (10,33,34).

Differential RNA display was directly performed with reciprocally subtracted cDNA plasmid libraries (E11 minus E11-NMT and E11-NMT minus E11). Compared with the subtraction of PCR-amplified cDNA in Hakvoort et al., the subtracted cDNA libraries used in this experiment are free from potential PCR artifacts and provide more stable and consistent sources for DDRT-PCR analyzes. In addition, three single anchored oligo dT 3' primers were used instead of two-base-anchored approach described by Hakvoort et al (32). To further streamline the DDRT-PCR procedure, reamplified cDNAs identified using RSDD were analyzed using the reverse Northern blotting procedure (35,36). cDNAs displaying differential expression by reverse Northern blotting were subsequently confirmed for true differential expression by Northern analysis. These modifications incorporated in the RSDD strategy result in an efficient approach for using subtractive hybridization

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and DDRT-PCR for identifying differentially expressed genes.

Methods

- 5 Total RNA from E11 and E11-NMT cells was isolated by the guanidinium isothiocyanate/CsCl centrifugation procedure and poly A⁺ RNA was purified with oligo(dT) cellulose chromatography (5). Two λ-ZAP cDNA libraries from E11 and E11-NMT mRNA's were constructed with λ-ZAP cDNA library Kits (Stratagene) following the manufacturer's protocol.
- 10 Reciprocal subtraction between E11 and E11-NMT libraries was performed and two subtracted cDNA libraries (E11 minus E11-NMT and E11-NMT minus E11) were constructed as described previously. Bacterial plasmid libraries from the subtracted λ-ZAP cDNA libraries were obtained by *in vivo* excision following the manufacturer's protocol (Stratagene) and the plasmids were isolated with Qiagen columns (Qiagen Inc.).
- 15 The purified plasmids of reciprocally subtracted cDNA libraries were directly subjected to differential display as in Liang et. al. (38) with minor modifications. The plasmids of reciprocally subtracted cDNA libraries were PCR-amplified with the combination of three single-anchor 20 3' primers (T₁₃ A, T₁₃ C or T₁₃ G) and 18 arbitrary 5' 25 10-mer primers obtained from Operon Technology Inc. (Alameda, CA. OPA 1-20 except OPA1 and 3). The 20 μl PCR reaction consisted of 10 mM Tris-HCl pH 8.4, 50 mM KCl, 1.5 mM MgCl₂, 2 μM each dNTP, 0.2 μM 5' arbitrary primer, 1 μM 3' anchor primer, 50 ng of plasmid of a subtracted 30 library, 10 μCi α-³⁵S-dATP (3000 Ci/mmol from Amersham) and 1 U of Taq DNA polymerase (Gibco BRL). The parameters of PCR were 30 sec at 95 C, 40 cycle of 30 sec at 95 C, 2 min. at 40 C and 30 sec at 72 C and additional 35 5 min. at 72 C. After the cycling, 10 μl of 95% formamide, 0.05% bromophenol blue and 0.05% xylene cyanol were added to each PCR reaction. The mixture was heated

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at 95 °C for 2 min and separated in a 5% denaturing DNA sequencing gel maintained at 50 °C. PCR reactions of plasmids from each subtracted library in a primer set were run side by side. Differentially amplified bands 5 from plasmids of each subtracted library were marked with an 18G needle through the film and cut out with a razor. The gel slice was put in 100 µl TE pH 8.0 and incubated at 4 °C overnight. After the incubation, the mixture was boiled for 5 min and microcentrifuged for two min. The 10 supernatant was collected and stored at -20 °C until reamplification. The band extract was reamplified with the same cycling parameters in a 50 µl reaction consisting of 10 mM Tris-HCl pH 8.4, 50 mM KCl, 1.5 mM MgCl₂, 20 µM each dNTP, 0.2 µM 5' arbitrary primer, 1 µM 15 3' anchor primer, 5 µl of band extract and 2.5 U of Tag DNA polymerase (Gibco BRL).

Differential expression of the reamplified DNA fragment was scrutinized by reverse Northern and Northern blot analyses. In reverse Northern analysis, after confirmation in a 1% agarose gel, the reamplified DNA fragment (10 µl of PCR reaction) was mixed with 90 µl TE and spotted on a positively charged Nylon membrane (Boehringer Mannheim) with a 96-well vacuum manifold. 20 The membrane was soaked with denaturing and neutralizing solution successively, and the spotted DNA was crosslinked to the membrane with a UV crosslinker (Stratagene). ³²P-labeled first strand cDNA was prepared by reverse transcription of total RNA. After heating at 25 70 °C for 10 min and quenching on ice for two min, 0.4 µM each T₁₃A, T₁₃G and T₁₃C and 10 µg total RNA mixture was added with 50 mM Tris-HCl, pH 8.3, 75 mM KCl, 3 mM MgCl₂, 10 mM DTT, 0.5 mM dATP, 0.5 mM dGTP, 0.5 mM dTTP, 0.02 mM dCTP, 0.5 µl RNase inhibitor (Gibco BRL), 100 µCi 30 dCTP (3000 Ci/mmol from Amersham) and 200 U Superscript RT II (Gibco BRL) in a final 25 µl reaction. The reaction mixture was incubated at 42 °C for one hr and at 35

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37 °C for 30 min after addition of 2 µl of RNase H (10U, Gibco BRL). The membrane was hybridized at 42 °C overnight in a 50% formamide hybridization solution. The hybridized membrane was washed at room temperature for 15
5 min with 2X SSC containing 0.1% SDS twice and at 55 °C for at least one hr with 0.1X SSC containing 0.1% SDS, successively. The membrane was probed with the ³²P-labeled cDNA of E11, stripped off and probed with ³²P-labeled cDNA of E11-NMT. The signal intensity of each
10 spot was normalized against that of GAPDH and compared between E11 and E11-NMT. Reamplified DNA fragments displaying differential expression levels ≥1.8-fold higher between the two cell types were selected and analyzed by Northern blotting analysis.

In Northern blot analysis, 10 µg of total RNA from E11 and E11-NMT cells were run side-by-side in a 1% agarose gel with formaldehyde and transferred to a positively charged Nylon membrane. Reamplification reaction (5 µl)
15 was ³²P-labeled with a multiprime labeling kit (Boehringer Mannheim) used to probe the membrane as described above. DNA fragments expressed differentially between E11 and E11-NMT in Northern blot analyses were cloned into the Eco RV site of the pZERo-2.1 cloning vector (Invitrogen) and sequenced.
20 In order to confirm differential expression, the cloned cDNA fragment was released by Eco RI -Xho I, ³²P-labeled and used to probe Northern blots as described above. Samples of RNAs from various E11 and E11-NMT derivatives displaying either a progressed or suppressed progression phenotype, based on nude mice tumorigenesis and soft agar cloning assays were analyzed.
25 These included E11, E11-NMT, CREF X E11-NMT F1 and F2 somatic cell hybrids (suppressed progression phenotype), CREF X E11-NMT R1 and R2 somatic cell hybrids (progression phenotype), E11 X E11-NMT A6 somatic cell hybrid (suppressed progression phenotype), E11 X E11-NMT A6TD tumor-derived somatic cell hybrid (progression
30 phenotype).

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phenotype), E11 X E11-NMT 3b somatic cell hybrid (suppressed progression phenotype), E11 X E11-NMT 2a (progression phenotype), E11-NMT AZA B1 and C1 5-azacytidine treated E11-NMT clones (suppressed progression phenotype), E11-ras R12 clone containing the Ha-ras oncogene (progression phenotype) and E11-HPV E6/E7 clone containing the human papilloma virus-18 E6 and E7 gene region (progression phenotype). Differential expression of the PEGen and PSGen genes in the various cell types was confirmed using ^{32}P -labeled probes and Northern hybridization analysis. After reconfirmation of differential expression, the plasmids containing the differentially expressed DNA fragments were sequenced by the dideoxy sequencing procedure.

15

Results and Discussion

Subtraction hybridization provides a direct means of enriching for unique cDNA species and eliminating common sequences between complex genomes. DDRT-PCR is a proven methodology for the rapid identification and cloning of differentially expressed sequences between cell types (3,4,22). In principle, subtraction hybridization combined with DDRT-PCR should reduce band complexity which often obscures the identification of differentially expressed genes and generates false positive signals (23,28). This strategy, RSDD, has been used to analyze genes differentially expressed during transformation progression. The differential RNA display pattern of E11 and E11-NMT cells using standard differential RNA display (DDRT-PCR) and RSDD is shown in Fig. 1 (Left Panel). As predicted, the differential RNA display pattern of RSDD was much less complex than that of DDRT-PCR. The majority of bands common to both cDNA samples were eliminated using RSDD. These experiments demonstrate that subtractive hybridization prior to differential RNA display is effective in simplifying display patterns

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permits the efficient identification of differentially expressed cDNAs. Since RSDD significantly reduced the number of bands displayed, single anchor oligo dT primers, that can increase band numbers, were successfully used in subsequent applications of the RSDD approach (Fig. 1; Right Panel). Using RSDD, 235 differentially displayed cDNAs in the E11/E11-NMT tumor progression model system were isolated.

Hakvoort et. al. (32) used a reciprocal subtraction approach to analyze gene expression changes resulting during liver regeneration following 70% hepatectomy, i.e., normal liver subtracted from partially hepatectomized regenerating liver and vice versa. Although some bands displayed apparent enrichment, the complexity of the display pattern did not show appreciable simplification. These results are in stark contrast to RSDD, which results in a clear delineation and simplification of differentially expressed amplified bands (Figs. 1). Although conceptually similar, RSDD is significantly more effective than the subtraction plus DDRT-PCR approach described by Hakvoort et al. (32). The improved efficiency of RSDD versus the Hakvoort et al. (32) approach can be attributed to several factors. The approach of Hakvoort et al. (32) is based on the subtraction procedure described by Wang and Brown (38). This approach involves multiple rounds of PCR-amplification prior to each round of subtractive hybridization. In contrast, RSDD involves a single round of reciprocal subtraction that does not involve PCR amplification (5,10). In this respect, the complicated display pattern observed by Hakvoort et al. (32) even after three or four rounds of subtraction might result from reduced subtraction efficiency, PCR artifacts or a combination of these problems. Increasing the number of reactions by using two-base pair anchored oligo dT primers did not reduce the complexity of displayed bands.

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(32). In these contexts, a critical component for the successful use of RSDD involves the use of an appropriate subtraction hybridization protocol, that can efficiently reduce cDNA complexity and generate stable populations of cDNAs for analysis.

Previous studies demonstrate that different gene cloning strategies, including DDRT-PCR, subtraction hybridization and electronic display, identify dissimilar differentially expressed genes (18). These results suggest that a single approach for gene identification may not identify the complete spectrum of differentially expressed genes (18). Similarly, RSDD and DDRT-PCR do not resolve the same differentially expressed bands (Fig. 1). Unique bands identified in DDRT-PCR that were differentially expressed when analyzed by Northern blotting were not the same as those found using RSDD and vise versa. These results are not surprising, since, as indicated above, subtraction hybridization and differential RNA display identified distinct differentially expressed genes. Apparently, specific differentially expressed genes are lost during subtraction hybridization and differential RNA display of subtracted cDNAs. On the basis of these considerations, it will be essential to use multiple gene discovery approaches to identify and clone the complete spectrum of differentially expressed genes.

DDRT-PCR can generate large numbers of differentially displayed bands making subsequent analysis both labor intensive and a daunting challenge. In order to reduce these limitations of DDRT-PCR, RSDD has been used in combination with reverse Northern analyses of isolated cDNAs. Gel extracted cDNA fragments were reamplified, dot-blotted on Nylon membranes and successively probed with reverse transcribed ³²P-cDNA from E11 or E11-NMT RNAs (Fig. 2). Signals were detected in 181 reamplified bands

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out of 235 (77%). This number is lower than that observed using DDRT-PCR (51 out of 54). However, this comparison may not be accurate since only four arbitrary primers were used for DDRT-PCR and fewer differentially expressed bands were detected and isolated. A possible reason for the high incidence of false positives in RSDD may be due to the existence of foreign plasmid-like DNA in the cDNAs and the inaccurate reading properties of DDRT-PCR.

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Table 1. Differentially Expressed cDNA Fragments Cloned by DDRT-PCR.

	Nomenclature	Identity	Homology
5	PEGen 41	To be determined	
10	PEGen 42	Novel	Novel
15	PEGen 43	Novel	Novel
20	PEGen 44	Novel	Novel
25	PEGen 45	Hoxall locus antisense	mouse 90%
30	PEGen 46	Glutamyl t-RNA synthetase	human 59%
35	PEGen 48	Novel	Novel
40	PEGen 50	Novel	Novel
45	PSGen 1	Supervillin	<i>B. taurus</i> 80%
50	PSGen 2	HTLV-1 Tax interacting protein	human 91%
55	PSGen 4	Proteasome activator	Rat 100%
60	PSGen 27	Novel	

The signal intensities of the various cDNAs in reverse Northern analysis were quantified and normalized against that of GAPDH, which remained unchanged in E11 and E11-NMT cells. The PEG-3 (PEGen-3) gene (10) was used as an additional control, to verify increased expression in E11-NMT versus E11 cells. In the reverse Northern

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analyses, PEGen-3 levels were 4-fold higher in E11-NMT than in E11 cells, which coincided with Northern blotting results, thereby demonstrating the concordance of reverse Northern and Northern assays. A \geq 1.8-fold differential cut-off (after normalization for GAPDH expression) was used to identify and isolate cDNA bands displaying modified expression in E11 versus E11-NMT cells. This resulted in the identification of 7 cDNAs with higher expression in E11 versus E11-NMT cells and 65 cDNAs with elevated expression in E11-NMT versus E11 cells. These results suggest that tumor progression in E11-NMT cells correlates with the increased expression of a large number of genes, whereas only a smaller subset of genes display decreased expression.

A problem present in DDRT-PCR, that is reduced but still can occur in RSDD, is the isolation of multiple cDNA species from what appears to be a single amplified band. When this occurs, these multiple species can produce spurious results when analyzed by reverse Northern analyses. For example, if two distinct species are isolated, one displaying modified expression and a second not displaying modified expression, an accurate estimate of differential expression will not be obtained by reverse Northern analysis. In this case, a number of potential false positives generated using reverse Northern analyses, may in reality not be false positives, but instead may represent multiple cDNAs. This problem may be ameliorated by performing single strand conformational polymorphism (SSCP) or reverse Northern analyses using cloned cDNA populations (39, 40).

The expression pattern of representative RSDD-derived cDNAs in E11 versus E11-NMT and in a more expanded E11/E11-NMT progression cell culture series is shown in Figs. 3 and 4, respectively. Reverse Northern results correlated well with Northern blots using E11 and

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E11-NMT (~80% concordance) or a larger panel of cells differentially displaying the progression phenotype, including progression negative, E11, CREF x E11-NMT F1, CREF X E11-NMT F2, E11 X E11-NMT A6, E11 X E11-NMT 3b, 5 E11-NMT Aza B1 and E11-NMT Aza C1, and progression positive E11-NMT, CREF X E11-NMT R1, CREF X E11-NMT R2, E11 X E11-NMT A6TD, E11 X E11-NMT IIa, E11-ras and E11-HPV E6/E7. Sequence analysis of the various 10 progression upregulated genes (PEGen) and progression suppressed genes (PSGen) identified both known and unknown genes (Table 2). Known PEGen genes included PEGen 7 (HPV16 E1BP), PEGen 8 (PFK-C), PEGen 21 (FIN 14) and PEGen 26 (poly ADP-ribose polymerase) and a known PSGen gene was PSGen 10 (ferritin heavy chain). Two 15 PEGen genes out of six were found to be novel (PEGen 14 and PEGen 24) and two PSGen genes out of three were found to be novel (PSGen 12 and PSGen 13) (Table 2).

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Table 2. Differentially Expressed cDNA Fragments
Cloned by RSDD

	Nomenclature	Identity	Homology
5	PEGen 7	HPV16 E1BP	Human 90%
	PEGen 8	PFK-C	Rat 100%
10	PEGen 13	Novel	Novel
	PEGen 14	Novel	Novel
	PEGen 15	Novel	Novel
15	PEGen 21	FIN 14	Mouse 94%
	PEGen 24	Novel	Novel
20	PEGen 26	Poly ADP-ribose Polymerase	Rat 100%
	PEGen 28	Novel	Novel
	PEGen 32	Novel	Novel
25	PSGen 10	Ferritin Heavy Chain	Rat 100%
	PSGen 12	Novel	Novel
30	PSGen 13	Novel	Novel
	PSGen 23	Novel	Novel

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	PSGen 24	Novel	Novel
	PSGen 25	Novel	Novel
5	PSGen 26	Novel	Novel
	PSGen 27	Novel	Novel
10	PSGen 28	Novel	Novel
	PSGen 29	Novel	Novel
15	PEGen 7 is expressed at ~ 5-fold higher levels in E11-NMT than in E11 cells. PEGen 7 is ~90% homologous to 16E1-BP, a cDNA encoding a protein identified using the yeast two-hybrid assay that interacts with human papillomavirus type 16 E1 protein (41). 16E1-BP encodes a 432aa protein of unknown function but does contain an ATPase signature motif (Gly-X ₄ -Gly consensus ATP binding motif at aa 179 through 186). 16E1-BP appears to be a form of TRIP13, a protein previously shown to bind thyroid hormone receptor in yeast two-hybrid assays. The role of PEGen 7/16E1-BP in the progression phenotype in the E11/E11-NMT progression model is not known. Additional studies are necessary to determine if this gene change is associative or causative of transformation progression.		
30	PEGen 8 is expressed at ~3- to 4- fold higher levels in E11-NMT than in E11 cells. PEGen 8 shows 100% homology to rat phosphofructokinase C (PFK-C) (42). PFK catalyzes the rate-limiting and committed step in glycolysis, the conversion of fructose 6-phosphate to fructose 1,6-biphosphate. Three subunit isozymes of PFK have been identified, that form homo- and heterotetramers with differing catalytic and allosteric properties. PFK-M is		

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specific for cardiac and skeletal muscle, PFK-L is expressed in many tissues but is most abundant in the liver and PFK-C is expressed in several brain regions and the anterior pituitary but not in liver, skeletal muscle, or several other human tissues. The cDNA of PFK-C isolated from a rat hypothalamic cDNA library is 2643 bp and encodes a protein of 765aa (42). In a recent study, Sanchez-Martinez and Aragon (43) demonstrated that PFK-C is the predominant form of PFK in ascites tumor cells (obtained from a transplantable mouse carcinoma of mammary origin), whereas PFK-L is most abundant in the normal mammary gland. These results suggest the interesting possibility that PFK-C might contribute to the malignant nature of specific target cells. The role of PEGen 8/PFK-C in progression in the E11/E11-NMT model remains to be determined.

PEGen 21 is expressed at ~3- to 4-fold higher levels in E11-NMT than in E11 cells. PEGen 21 displays ~94% homology with the fibroblast growth factor-4 inducible gene FIN-14 (44). FIN-14 is a novel cDNA of unknown function that hybridizes with a 4.5 kb mRNA that is induced 4-fold in NIH3T3 mouse cells following treatment with FGF-4. The induction of FIN-14 occurs late (18 hr) after treatment with FGF-4 and does not occur when cells are treated for 18 hr with FGF-4 in the presence of cycloheximide (44). These results confirm that FIN-14 encodes a late-inducible gene. Moreover, nuclear run-on assays document that FIN-14 is transcriptionally activated in NIH3T3 cells following growth factor stimulation. Tissue distribution studies indicate expression of a single mRNA species in the kidney with low levels of expression observed in several other tissues including testis and thymus. Mouse embryogenesis studies indicate that FIN-14 expression occurs constitutively in mouse embryos between day 10.5 and 15.5. Unlike NIH3T3, FIN-14 was constitutively expressed in PC12 cells and its level

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did not vary appreciably in response to growth factor stimulation. The role of PEGen 21/FIN-14 in progression in E11/E11-NMT model system is not currently known.

5 The PSGen cDNAs, PSGen-12 and PSGen-13, consist of sequences without homology to those presently reported in various DNA databases. Expression of these cDNAs is ~3- to 4-fold higher in E11 versus E11-NMT cells (Fig. 3). It is not currently known whether these genes simply
10 correlate with or functionally regulate the progression phenotype. The identification of full-length cDNAs for PSGen-12 and PSGen-13 are in progress and once identified experiments can be conducted to directly define the role of these PSGen's in cancer progression.

15 We presently demonstrate that a modified differential RNA display technique, RSDD, can efficiently identify differentially expressed cDNAs. As predicted, subtractive hybridization prior to differential RNA display greatly reduces band complexity, a problem encountered in standard DDRT-PCR in which RNA samples are directly analyzed without subtraction. Unlike a previous report using subtracted cDNAs processed through successive rounds of PCR (32,45), common bands were
20 eliminated using reciprocally subtracted cDNA libraries that had not been processed using PCR. In addition to subtraction hybridization, the discovery of differentially expressed genes was further streamlined by using reverse Northern analyses with isolated cDNAs.
25 With 3 single anchored oligo dT primers and 18 arbitrary 5' primers, 72 bands were identified that displayed differential expression using reverse Northern analysis. Currently, 40 of these cDNA species have been analyzed by Northern blotting and found to display differential expression in E11 versus E11-NMT cells. Subsequent studies with the majority of these RSDD cDNAs demonstrated coordinated expression with the progression
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phenotype in a large panel of unprogressed and progressed transformed cells. Current sequence analysis of the cloned cDNA fragments revealed 9 different genes, including 4 novel genes not reported in recent DNA databases. RSDD represents a method of choice either as a more efficient and less time consuming modification of the differential RNA display strategy or as a screening methodology for identifying differentially expressed genes in reciprocally subtracted cDNA libraries.

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Second Series of Experiments

Presently described is a RSDD approach that efficiently and consistently reduces the complexity of DDRT-PCR and results in the identification and cloning of genes displaying anticipated differential expression. The model used for RSDD was an adenovirus-transformed rat embryo cell line, E11, that acquires an aggressive oncogenic progression phenotype when injected into athymic nude mice and reestablished in cell culture (E11-NMT) (6,26,27). Injection of E11 cells into nude mice results in tumors in 100% of animals with a tumor latency time of approximately 35 to 40 days, whereas E11-NMT cells form tumors in 100% of nude mice with a tumor latency time of 15 to 20 days (6,26,27). Additionally, E11 cells form colonies in agar with an efficiency of ~3 %, whereas E11-NMT display an agar cloning efficiency of >30% (6,26,27). The increased tumorigenicity and enhanced anchorage independence phenotypes are key indicators of tumor progression in the E11/E11-NMT model system (6,26,27). RSDD has resulted in the identification and cloning of genes displaying elevated expression in progressed tumor cells (progression elevated gene, PEGen) and suppressed expression in progressed tumor cells (progression suppressed gene, PSGen).

MATERIALS AND METHODS

RNA isolation and cDNA library construction. Total RNA from E11 and E11-NMT cells was isolated by the guanidinium isothiocyanate/CsCl centrifugation procedure and poly(A)⁺ RNA was purified with oligo(dT) cellulose chromatography(5). Two λ-ZAP cDNA libraries from E11 and E11-NMT mRNAs were constructed with λ-ZAP cDNA library kits (Stratagene) following the manufacturer's protocol. Reciprocal subtraction between E11 and E11-NMT libraries was performed and two subtracted cDNA libraries (E11 minus E11-NMT and E11-NMT minus E11) were constructed as

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described(5,6). Plasmid cDNA libraries from the subtracted λ -ZAP cDNA libraries were obtained by in vivo excision following the manufacturer's protocol (Stratagene) and the plasmids were isolated with Qiagen columns (Qiagen, Chatsworth, CA.).

RSDD methodology. The purified plasmids of reciprocally subtracted cDNA libraries were directly subjected to differential display as in Liang et al. (28) with minor modifications. The plasmids of reciprocally subtracted cDNA libraries were PCR-amplified with the combination of three single-anchor 3' primers ($T_{13}A$, $T_{13}C$ or $T_{13}G$) and 18 arbitrary 5' 10-mer primers obtained from Operon Technology Inc. (Alameda, CA. OPA 1-20 except OPA1 and 3). The 20 μ l PCR reaction consisted of 10 mM Tris-HCl (pH 8.4), 50 mM KCl, 1.5 mM MgCl₂, 2 μ M each dNTP, 0.2 μ M 5' arbitrary primer, 1 μ M 3' anchor primer, 50 ng of plasmid of a subtracted library, 10 μ Ci α -³⁵S-dATP (3,000 Ci/mmol from Amersham) and 1 unit of Taq DNA polymerase (Gibco/BRL). The parameters of PCR were 30 sec at 95°C, 40 cycles of 30 sec at 95°C, 2 min at 40°C and 30 sec at 72°C and additional 5 min. at 72°C. After the cycling, 10 μ l of 95% formamide, 0.05% bromophenol blue and 0.05% xylene cyanol were added to each PCR reaction. The mixture was heated at 95°C for 2 min and separated in a 5% denaturing DNA sequencing gel maintained at 50°C. PCR reactions of plasmids from each subtracted library in a primer set were run side by side. Differentially amplified bands from plasmids of each subtracted library were marked with 18G needle through the film and cut out with a razor. The gel slice was put in 100 μ l TE (pH 8.0) and incubated at 4°C overnight. After the incubation, the mixture was boiled for 5 min and microcentrifuged for two min. The supernatant was collected and stored at -20°C until reamplification. The band extract was reamplified with the same cycling parameters in a 50 μ l reaction consisting of 10 mM Tris-HCl (pH 8.4), 50 mM KCl, 1.5 mM

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MgCl₂, 20 μM each dNTP, 0.2 μM 5' arbitrary primer, 1 μM 3' anchor primer, 5μl of band extract and 2.5 units of Taq DNA polymerase (Gibco/BRL).

5 **Reverse Northern Blotting Procedure.** Differential expression of the reamplified DNA fragment was scrutinized by reverse Northern and Northern blot analyses. In reverse Northern analysis, after confirmation in a 1% agarose gel, the reamplified DNA fragment (10 μl of PCR reaction) was mixed with 90 μl TE and spotted on a positively charged Nylon membrane (Boehringer Mannheim) with a 96-well vacuum manifold. The membrane was soaked with denaturing and neutralizing solution successively, and the spotted DNA was crosslinked to the membrane with a UV crosslinker (Stratagene). ³²P-labeled first strand cDNA was prepared by reverse transcription of total RNA. After heating at 70°C for 10 min and quenching on ice for two min, 0.4 μM each T₁₃A, T₁₃G and T₁₃C and 10 μg total RNA mixture was added with 50 mM Tris-HCl, (pH 8.3), 75 mM KCl, 3 mM MgCl₂, 10 mM DTT, 0.5 mM dATP, 0.5 mM dGTP, 0.5 mM dTTP, 0.02 mM dCTP, 0.5 μl RNase inhibitor (Gibco/BRL), 100 μCi dCTP (3,000 Ci/mmol from Amersham) and 200 units Superscript RT II (Gibco/BRL) in a final 25 μl reaction. The reaction mixture was incubated at 42°C for one hour and at 37°C for 30 min after addition of 2 μl of RNase H (10 units, Gibco/BRL). The membrane was hybridized at 42°C overnight in a 50% formamide hybridization solution. The hybridized membrane was washed at room temperature for 15 min with 2X standard saline citrate containing 0.1% SDS twice and at 55°C for at least one hour with 0.1X Standard Saline Citrate containing 0.1% SDS, successively. The membrane was probed with the ³²P-labeled cDNA of E11, striped off and probed with ³²P-labeled cDNA of E11-NMT. The signal intensity of each spot was normalized against that of glyceraldehyde-3-phosphate dehydrogenase and compared between E11 and E11-NMT. Reamplified DNA

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fragments displaying differential expression levels ≥ 1.8 -fold higher between the two cell types were selected and analyzed by Northern blotting analysis.

5 **Northern Blotting Analysis.** In Northern blot analysis, 10
μg of total RNA from E11 and E11-NMT cells were run
side-by-side in a 1% agarose gel with formaldehyde and
transferred to a positively charged Nylon membrane.
10 Reamplification reaction (5 μl) was ³²P-labeled with a
multiprime labeling kit (Boehringer Mannheim) used to
probe the membrane as described above. DNA fragments
expressed differentially between E11 and E11-NMT in
Northern blot analyses were cloned into the EcoRV site of
the pZEr0-2.1 cloning vector (Invitrogen) and sequenced.

To confirm differential expression, the cloned cDNA fragment was released by EcoRI-XbaI, ³²P-labeled and used to probe Northern blots as described above. Samples of RNAs from various E11 and E11-NMT derivatives displaying either a progressed or suppressed progression phenotype, based on nude mice tumorigenesis and soft agar cloning assays were analyzed. These included E11, E11-NMT, CREF x E11-NMT F1 and F2 somatic cell hybrids (suppressed progression phenotype), CREF x E11-NMT R1 and R2 somatic cell hybrids (progression phenotype), E11 x E11-NMT A6 somatic cell hybrid (suppressed progression phenotype), E11 x E11-NMT A6TD tumor-derived somatic cell hybrid (progression phenotype), E11 x E11-NMT 3b somatic cell hybrid (suppressed progression phenotype), E11 x E11-NMT IIa (progression phenotype), E11-NMT AZA B1 and C1 5-azacytidine treated E11-NMT clones (suppressed progression phenotype), E11-Ras R12 clone containing the Ha-ras oncogene (progression phenotype) and E11-HPV E6/E7 clone containing the human papilloma virus-18 E6 and E7 gene region (progression phenotype). Differential expression of the PEGen and PSGen genes in the various cell types was confirmed using ³²P-labeled probes and

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northern hybridization analysis. After reconfirmation of differential expression, the plasmids containing the differentially expressed DNA fragments were sequenced by the dideoxy sequencing procedure.

5

RESULTS AND DISCUSSION

Subtraction hybridization provides a direct means of enriching for unique cDNA species and eliminating common sequences between complex genomes(7,18). DDRT-PCR is a proven methodology for the rapid identification and cloning of differentially expressed sequences between cell types (1,2,28). In principle, subtraction hybridization combined with DDRT-PCR should reduce band complexity which often obscures the identification of differentially expressed genes and generates false positive signals (21,29). RSDD has been used to analyze genes differentially expressed during transformation progression (Fig. 28). Differential RNA display was directly performed with reciprocally subtracted cDNA 10 plasmid libraries (E11 minus E11-NMT and E11-NMT minus E11) that had not been subjected to PCR. Three single anchored oligo dT 3' primers were used for subsequent amplification prior to display. To further streamline the DDRT-PCR procedure, reamplified cDNAs identified using 15 RSDD were analyzed using the reverse Northern blotting procedure (30,31). cDNAs displaying differential expression by reverse Northern blotting were subsequently confirmed for true differential expression by Northern 20 analysis.

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The differential RNA display pattern of E11 and E11-NMT cells using standard differential RNA display (DDRT-PCR) and RSDD is shown in Fig. 1 (Left Panel). The differential RNA display pattern of RSDD is much less 30 complex than that of DDRT-PCR. These experiments demonstrate that subtractive hybridization prior to differential RNA display is effective in simplifying

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display patterns permitting the efficient identification of differentially expressed cDNAs. Since RSDD significantly reduced the number of bands displayed, single anchor oligo dT primers, that can increase band numbers, were successfully used in subsequent applications of the RSDD approach (Fig. 1; Right Panel). Using RSDD, 234 differentially displayed cDNAs in the E11/E11-NMT tumor progression model system were isolated.

Hakvoort et al. (25) used a reciprocal subtraction approach to analyze gene expression changes resulting during liver regeneration following 70% hepatectomy, i.e., normal liver subtracted from partially hepatectomized regenerating liver and vice versa. Although some bands displayed apparent enrichment, the complexity of the display pattern did not show appreciable simplification. In contrast, RSDD results in a clearer delineation and simplification of differentially expressed amplified bands (Figs. 1).

Although conceptually similar, RSDD is significantly more effective than the subtraction plus DDRT-PCR approach described by Hakvoort et al. (25) The reasons for the improved efficiency of RSDD versus the Hakvoort et al. (25) approach are not known. One possibility is that the differences between the experimental approaches may reflect the subtraction hybridization strategies employed. The approach of Hakvoort et al. (25) is based on the subtraction procedure described by Wang and Brown (32). This approach uses multiple rounds of PCR-amplification prior to each round of subtractive hybridization. In contrast, RSDD involves a single round of reciprocal subtraction without intermediate amplification (5,6). In this respect, the complicated display pattern observed by Hakvoort et al. (25) even after three or four rounds of subtraction might result from reduced subtraction efficiency, PCR artifacts or a combination of these problems. Increasing the number of reactions by using two-base pair anchored oligo dT

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primers did not reduce the complexity of displayed bands (25). In these contexts, a critical component for the successful use of RSDD involves the use of an appropriate subtraction hybridization protocol, which can efficiently reduce cDNA complexity and generate stable populations of cDNAs for analysis.

Previous studies demonstrate that different gene cloning strategies, including DDRT-PCR, subtraction hybridization and electronic display, identify distinct subsets of differentially expressed genes (18). These results suggest that a single approach for gene identification may not identify the complete spectrum of differentially expressed genes. Similarly, RSDD and DDRT-PCR do not resolve the same differentially expressed bands (Fig. 1). Unique bands identified in DDRT-PCR that were differentially expressed when analyzed by Northern blotting were not the same as those found using RSDD and vice versa (data not shown). These results are not surprising, since, as indicated above, subtraction hybridization and differential RNA display identified distinct differentially expressed genes (18). Apparently, specific differentially expressed genes are lost during subtraction hybridization and differential RNA display of subtracted cDNAs. On the basis of these considerations, it will be essential to use multiple gene discovery approaches to identify and clone the complete spectrum of differentially expressed genes.

DDRT-PCR can generate large numbers of differentially displayed bands making subsequent analysis both labor intensive and a daunting challenge. In order to reduce these limitations of DDRT-PCR, RSDD has been used in combination with reverse Northern analyses of isolated cDNAs. Gel extracted cDNA fragments were reamplified, dot-blotted on Nylon membranes and successively probed with reverse transcribed ³²P-cDNA from E11 or E11-NMT RNAs

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(Fig. 2). Signals were detected in 181 reamplified bands out of 234 (77%).

The signal intensities of the various cDNAs in reverse Northern analysis were quantified and normalized against that of GAPDH, which remained unchanged in E11 and E11-NMT cells. Progression elevated gene-3 (PEG-3) (6) was used as an additional control, to verify increased expression in E11-NMT versus E11 cells. In the reverse Northern analyses, PEG-3 levels were 4-fold higher in E11-NMT than in E11 cells, which coincided with Northern blotting results, thereby demonstrating the concordance of reverse Northern and Northern assays. A ≥ 1.8 -fold differential cut-off (after normalization for GAPDH expression) was used to identify and isolate cDNA bands displaying modified expression in E11 versus E11-NMT cells. This resulted in the identification of 7 cDNAs with higher expression in E11 versus E11-NMT cells and 65 cDNAs with elevated expression in E11-NMT versus E11 cells. These results suggest that tumor progression in E11-NMT cells correlates with increased expression of a large number of genes, whereas only a smaller subset of genes display decreased expression.

A problem frequently encountered in DDRT-PCR, that is reduced but still can occur in RSDD, is the isolation of multiple cDNA species from what appears to be a single amplified band. When this occurs, these multiple species can produce spurious results when analyzed by reverse Northern analyses. For example, if two distinct species are isolated, one displaying modified expression and a second not displaying modified expression, an accurate estimate of differential expression will not be obtained by reverse Northern analysis. In this case, a number of potential false positives generated using reverse Northern analyses, may in reality not be false positives, but instead may represent multiple cDNAs. By performing

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single strand conformational polymorphism (SSCP) or reverse Northern analyses using cloned cDNA populations (33,34) this problem can be ameliorated.

5 The expression pattern of representative RSDD-derived cDNAs in E11 versus E11-NMT and in a more expanded E11/E11-NMT progression cell culture series is shown in Figs. 29 and 30, respectively. Reverse Northern results correlated well with Northern blots using E11 and E11-NMT (~75% concordance) or a larger panel of cells differentially displaying the progression phenotype, including progression negative E11, CREF x E11-NMT F1 and F2, E11 x E11-NMT A6, E11 x E11-NMT 3b, E11-NMT Aza B1 and Aza C1 cells, and progression positive E11-NMT, CREF x E11-NMT R1 and R2, E11 x E11-NMT A6TD, E11 x E11-NMT IIa, E11-Ras R12 and E11-HPV E6/E7 cells. Sequence analysis of the various PEGen cDNAs identified both unknown and known genes (Table 3). Five of 10 PEGen cDNAs (50%) were classified as novel sequences since no matches were found in current DNA databases. Novel PEGen cDNAs include, PEGen 13, 14, 24, 28 and 32. Known PEGen genes included PEGen 7 (human papilloma virus-16 early region 1 binding protein; HPV16 E1BP), PEGen 8 (phosphofructokinase kinase C; PFK-C), PEGen 21 (a fibroblast growth factor-4 inducible gene; FIN 14), PEGen 26 (poly ADP-ribose polymerase) and PEGen 30 (rat espl homology). In the case of the PSGen cDNAs, six of six (100%) were novel, including PSGen 12, 13, 26, 27, 28 and 29 (Table 3).

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Table 3. PEGen and PSGen genes isolated using RSDD.

	Nomenclature ^a (%) ^c	Identity ^b	Homology
	PEGen 7	Human HPV16 E1BP	90
5	PEGen 8	Rat phospho-fructokinase C' (PFK-C) Unknown	100 Novel
	PEGen 13	Unknown	Novel
	PEGen 14	Unknown	Novel
	PEGen 21	Murine FIN 14	94
10	PEGen 24	Unknown	Novel
	PEGen 26	Rat poly ADP-ribose polymerase	100
	PEGen 28	Unknown	Novel
	PEGen 30	Rat esp1	98
15	PEGen 32	Novel	Novel
	PSGen 12	Unknown	Novel
	PSGen 13	Unknown	Novel
	PSGen 26	Unknown	Novel
	PSGen 27	Unknown	Novel
20	PSGen 28	Unknown	Novel
	PSGen 29	Unknown	Novel

25 ^aPEGen are progression elevated genes that display elevated expression in E11-NMT versus E11 cells. PSGen are progression suppressed genes that display elevated expression in E11 versus E11-NMT cells.

30 ^bSequences have compared with reported genes in various DNA data bases (including GenBank and EMBL) and identification with known genes are indicated. Genes without homology to currently reported genes are indicated as unknown.

35 ^cpercentage homology with known sequences, either human, rat or mouse is indicated.

Where no homology exists the cDNA is considered novel.

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PEGen 7 is expressed at ~ 4-fold higher levels in E11-NMT than in E11 cells. PEGen 7 is ~98% homologous to 16E1-BP, a cDNA encoding a protein identified using the yeast 5 two-hybrid assay that interacts with human papillomavirus type 16 E1 protein (35). 16E1-BP encodes a 432aa protein of unknown function but does contain an ATPase signature motif (Gly-X₄-Gly consensus ATP binding motif at aa 179 through 186). 16E1-BP appears to be a form of TRIP13, a 10 protein previously shown to bind thyroid hormone receptor in yeast two-hybrid assays. The role of PEGen 7/16E1-BP in the progression phenotype in the E11/E11-NMT progression model is not known. Additional studies are necessary to determine if this gene change is associative 15 or causative of transformation progression.

PEGen 8 is expressed at ~3- to 4- fold higher levels in E11-NMT than in E11 cells. PEGen 8 shows 100% homology to rat phosphofructokinase C (PFK-C) (36). PFK catalyzes the 20 rate-limiting and committed step in glycolysis, the conversion of fructose 6-phosphate to fructose 1,6-biphosphate. Three subunit isozymes of PFK have been identified, that form homo- and heterotetramers with differing catalytic and allosteric properties. PFK-M is 25 specific for cardiac and skeletal muscle, PFK-L is expressed in many tissues but is most abundant in the liver and PFK-C is expressed in several brain regions and the anterior pituitary but not in liver, skeletal muscle, or several other human tissues. The cDNA of PFK-C isolated from a rat hypothalamic cDNA library is 2643 bp 30 and encodes a protein of 765aa (-36). In a recent study Sanchez-Martinez and Aragon (37), demonstrated that PFK-C is the predominant form of PFK in ascites tumor cells (obtained from a transplantable mouse carcinoma of 35 mammary origin), whereas PFK-L is most abundant in the normal mammary gland. These results suggest the interesting possibility that PFK-C might contribute to the malignant nature of specific target cells. The role

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presently reported of PEGen 8/PFK-C in progression in the E11/E11-NMT model remains to be determined.

PEGen 21 is expressed at ~3- to 4-fold higher levels in
5 E11-NMT than in E11 cells. PEGen 21 displays ~98%
homology with the fibroblast growth factor-4 inducible
gene FIN-14 (38). FIN-14 is a novel cDNA of unknown
function that hybridizes with a 4.5 kb mRNA that is
induced 4-fold in NIH 3T3 mouse cells following treatment
10 with FGF-4. The induction of FIN-14 occurs late (18 hr)
after treatment with FGF-4 and does not occur when cells
are treated for 18 hr with FGF-4 in the presence of
cycloheximide (38). These results confirm that FIN-14
encodes a late-inducible gene. Moreover, nuclear run-on
15 assays document that FIN-14 is transcriptionally
activated in NIH 3T3 cells following growth factor
stimulation. Tissue distribution studies indicate
expression of a single mRNA species in the kidney with
low levels of expression observed in several other
20 tissues including testis and thymus. Mouse embryogenesis
studies indicate that FIN-14 expression occurs
constitutively in mouse embryos between day 10.5 and
15.5. Unlike NIH 3T3, FIN-14 was constitutively expressed
25 in PC12 cells and its level did not vary appreciably in
response to growth factor stimulation. The role of PEGen
21/FIN-14 in progression in E11/E11-NMT model system is
not currently known.

PEGen 26 is expressed at ~3- to 4-fold higher levels in
30 E11-NMT than in E11 cells. This cDNA is identical to rat
poly(ADP-ribose) polymerase (PARP) (39). PARP contributes
to the ability of eukaryotic cells to contend with both
environmental and endogenous genotoxic agents (40). PARP
is a nuclear enzyme that binds to DNA breaks and then
35 catalyzes the covalent modification of acceptor proteins
with poly(ADP-ribose) (39,40). PARP activity contributes
to the recovery of proliferating cells from DNA damage

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and to the maintenance of genomic stability, which may be regulated by effects on chromatin structure, DNA base-excision repair and cell cycle regulation (39,40). The role of PEGen 26/PARP in mediating the progression phenotype is not currently known. However, since cancer is a progressive disease characterized by the accumulation of genetic alterations in the evolving tumor (6), it is tempting to speculate that overexpression of PEGen 26/PARP in E11-NMT may facilitate the ability of these aggressive cancer cells to maintain genomic stability during cancer progression. In this context, PEGen 26/PARP may be an integral component of progression. This hypothesis is readily testable. PEGen 30 is expressed at 2- to 3-fold higher levels in E11-NMT than in E11 cells. This cDNA displays ~98.5% homology to rat esp1 (41). Rat esp1 encodes a 24-kDa nuclear protein which is the rat homologue of Drosophila Enhancer of split., a gene involved in ventral ectodermal development in Drosophila (41). PEGen 30 appears to be a homologue of esp1, since the message detected in E11 and E11-NMT cells (~4 kb) is larger in size than the reported esp1 transcript (1.3 kb)(41). The role of PEGen 30/esp1 in tumor progression in E11/E11-NMT model system remains to be determined.

The PSGen cDNAs, 12, 13, 26, 27, 28 and 29, consist of sequences without homology to those in various DNA databases. Expression of PSGen 12 and PSGen 13 cDNAs is ~3- to 4-fold higher in E11 versus E11-NMT cells (Fig. 29). It is not currently known whether these genes simply correlate with or functionally regulate the progression phenotype. The identification of full-length cDNAs for PSGen-12 and PSGen-13, as well as the other novel PSGen and PEGen cDNAs, are in progress and once isolated experiments can be conducted to directly define the role of these progression-related genes in cancer progression.

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Presently demonstrated is a modified gene-identification and gene-cloning technique, RSDD, that can efficiently identify differentially expressed cDNAs. As predicted, subtractive hybridization prior to differential RNA display greatly reduces band complexity, a problem encountered in standard DDRT-PCR in which RNA samples are directly analyzed without subtraction. Unlike a previous report using subtracted cDNAs processed through successive rounds of PCR (25, 42), common bands were eliminated using reciprocally subtracted cDNA libraries that had not been processed using PCR. In addition to subtraction hybridization, the discovery of differentially expressed genes was further streamlined by using reverse Northern analyses with isolated cDNAs. With 3 single anchored oligo dT primers and 18 arbitrary 5' primers, 72 bands were identified that displayed differential expression using reverse Northern analysis. Currently, 38 cDNA species have been analyzed by Northern blotting and 31 (~82%) displayed differential expression in E11 versus E11-NMT cells. Sequence analysis of the cloned cDNA fragments revealed 16 different genes, including 11 novel genes not reported in recent DNA databases. RSDD represents a method of choice either as a more efficient and less time consuming modification of the differential RNA display strategy or as a screening methodology for identifying differentially expressed genes in reciprocally subtracted cDNA libraries. Moreover, the ability of RSDD to identify differentially expressed genes that are dissimilar to those recognized using standard DDRT-PCR or subtraction hybridization indicates that this approach will be a valuable adjunct in cloning the complete repertoire of differentially expressed gene changes occurring between complex genomes.

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What is claimed is:

1. A method for identifying differentially expressed nucleic acids between two samples, comprising:
 - 5 a. selecting a first and second nucleic acid sample, wherein the nucleic acid samples contain a repertoire of nucleic acids;
 - b. performing reciprocal subtraction between the nucleic acid samples to produce two subtracted nucleic acid samples;
 - 10 c. amplifying the two subtracted nucleic acid samples; and
 - d. comparing the two subtracted nucleic acid samples to identify differentially expressed nucleic acids.
2. A method for identifying differentially expressed nucleic acids between two samples, comprising:
 - 20 a. selecting a first and second nucleic acid sample, wherein the nucleic acid samples contain a repertoire of nucleic acids;
 - b. amplifying the two nucleic acid samples;
 - c. performing reciprocal subtraction between the amplified nucleic acid samples to produce two subtracted nucleic acid samples; and
 - 25 d. comparing the two subtracted nucleic acid samples to identify differentially expressed nucleic acids.
3. The method of claim 2, wherein the two subtracted nucleic acid samples from step c are amplified prior to the comparing of step d.
- 35 4. The method of claim 1 or 2, wherein the each of the nucleic acid samples comprises a library of nucleic acids.

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5. The method of claim 1 or 2, wherein the nucleic acid samples are mRNA or cDNA derived from mRNA.
5. The method of claim 1 or 2, wherein the nucleic acid samples are obtained from total RNA from E11 and E11-NMT cells.
10. The method of claim 1 or 2, wherein the first and second nucleic acid samples are obtained from cells that differ in their exposure to external factors or in their gene expression.
15. The method of claim 1 or 2, wherein the first and second nucleic acid samples are obtained from cells in different developmental stages.
9. The method of claim 1 or 2, wherein the amplifying of step (d) comprises PCR amplification.
20. 10. The method of claim 9, wherein the PCR amplification uses a set of random primers.
25. 11. The method of claim 9, wherein the 3' primer used in the PCR amplification is a single anchor oligo dT 3' primer.
12. The method of claim 9, wherein the 5' primer is an arbitrary primer.
30. 13. The method of claim 1 or 2, wherein the comparing of step (e) comprises using a gel to separate the nucleic acids from both of the libraries.
35. 14. The method of claim 1 or 2, further comprising PCR amplifying the first and second nucleic acid samples.

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15. The method of claim 1 or 2, further comprising reamplifying differentially expressed nucleic acids.
- 5 16. The method of claim 1 or 2, wherein the comparing of step (e) comprises comparing the quantities of the two amplified differentially expressed nucleic acids.
- 10 17. The method of claim 1 or 2, wherein differences in the quantities of nucleic acid between the two subtracted libraries are electronically quantified.
- 15 18. The method of claim 1 or 2, wherein the libraries of step (b) are constructed with λ-ZAP cDNA library kits.
- 20 19. The isolated nucleic acid identified by the method of claim 1 or 2, wherein the nucleic acid was not previously known.
- 25 20. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PSGen 12.
- 30 21. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PSGen 13.
22. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PSGen 23.
- 35 23. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PSGen 24.
24. The isolated nucleic acid of claim 19, wherein the

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isolated nucleic acid is the nucleic acid designated
PSGen 25.

25. The isolated nucleic acid of claim 19, wherein the
5 isolated nucleic acid is the nucleic acid designated
PSGen 26.
26. The isolated nucleic acid of claim 19, wherein the
10 isolated nucleic acid is the nucleic acid designated
PSGen 27.
27. The isolated nucleic acid of claim 19, wherein the
isolated nucleic acid is the nucleic acid designated
PSGen 28.
- 15 28. The isolated nucleic acid of claim 19, wherein the
isolated nucleic acid is the nucleic acid designated
PSGen 29.
- 20 29. The isolated nucleic acid of claim 19, wherein the
isolated nucleic acid is the nucleic acid designated
PEGen 13.
- 25 30. The isolated nucleic acid of claim 19, wherein the
isolated nucleic acid is the nucleic acid designated
PEGen 14.
- 30 31. The isolated nucleic acid of claim 19, wherein the
isolated nucleic acid is the nucleic acid designated
PEGen 15.
- 35 32. The isolated nucleic acid of claim 19, wherein the
isolated nucleic acid is the nucleic acid designated
PEGen 24.
33. The isolated nucleic acid of claim 19, wherein the
isolated nucleic acid is the nucleic acid designated

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PEGen 28.

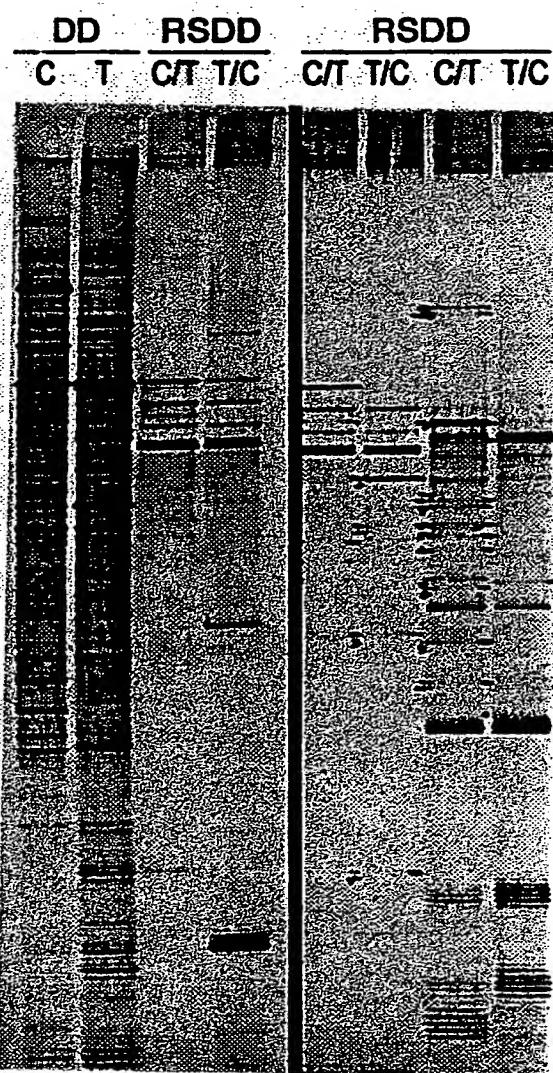
34. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PEGen 32.
- 5
35. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PEGen 42.
- 10
36. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PEGen 43.
- 15
37. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PEGen 44.
- 20
38. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PEGen 48.
- 25
39. The isolated nucleic acid molecule of claim 19 which comprises:
- (a) one of the nucleic acid sequences as set forth in Figure 35;
- (b) a sequence being degenerated to a sequence of
(a) as a result of the genetic code;
- 30
- (c) a sequence encoding one of the amino acid sequences as set forth in Figure 35.
- (d) a sequence of at least 12 nucleotides capable of specifically hybridizing to the sequence of
(a), (b) or (c)
- 35

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40. A purified polypeptide comprising one of the amino acid sequence as set forth in Figure 35.

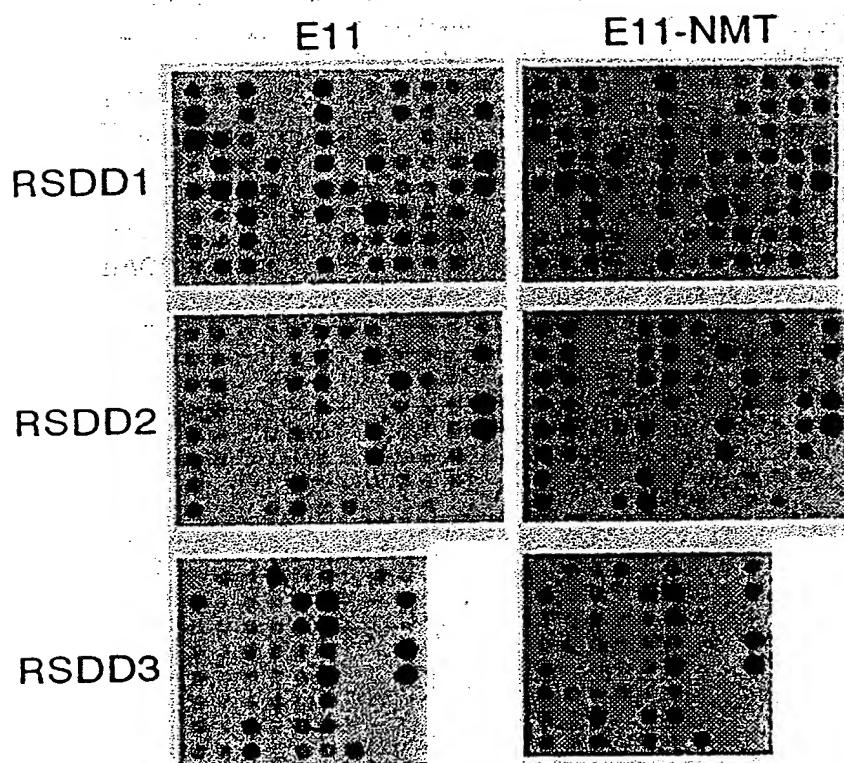
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FIG. 1

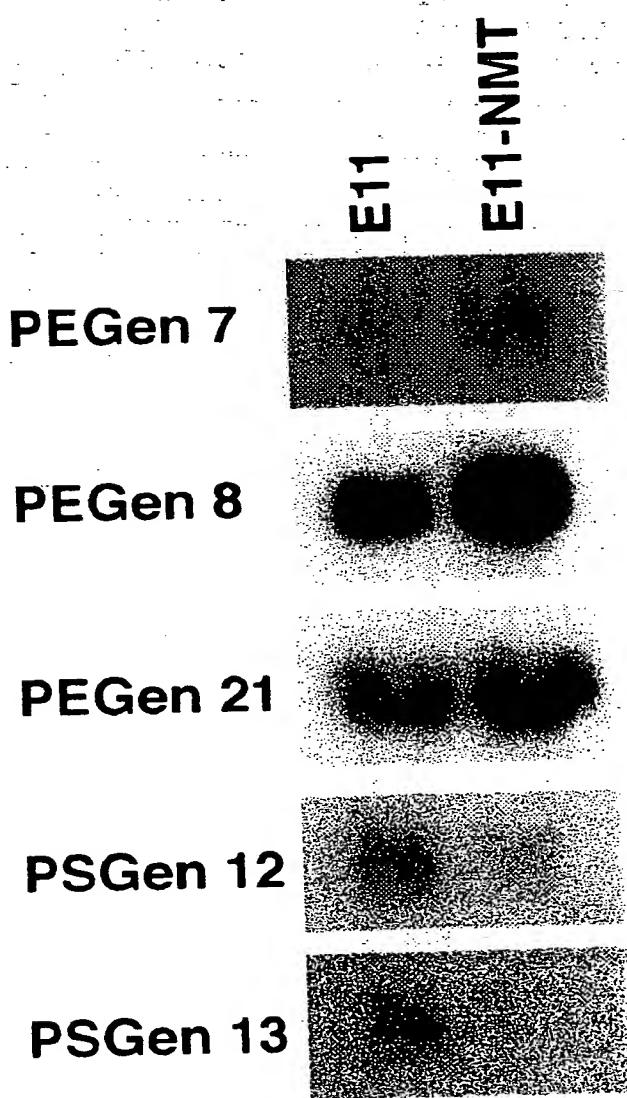


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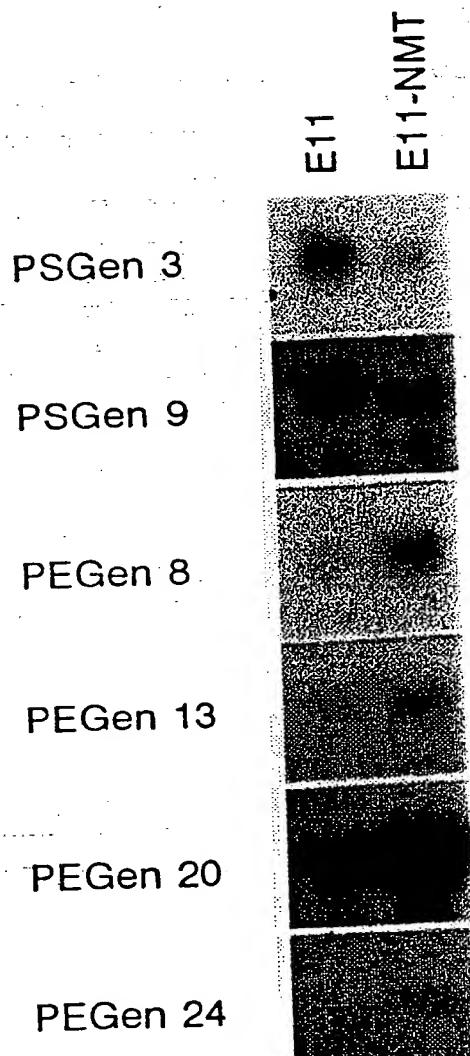
FIG. 2

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FIG. 3A

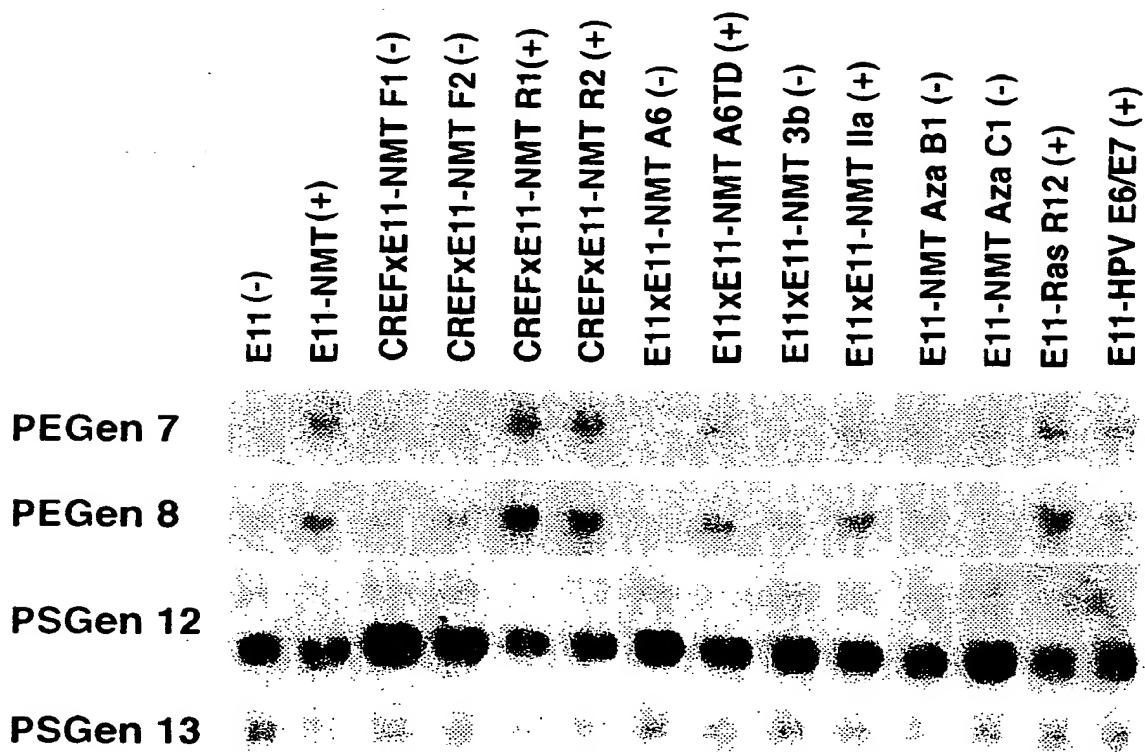
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FIG. 3B



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FIG. 4



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FIG. 5

PEGen 7-90% homology to human HPV16 E1BP

TAAANCGGTG GTACTGCTGC ACGGTCCCTCC GGGTACTGGGA AAGACATCCC
 TTTGTAAGGC ATTAGCCCCAG AAAACTGACCA TCAGACTGTC AACAGGGTAC
 CGGTATGGCC AGTTAATTGA AATAAACAGC CACAGCCTAT TTTCTAAGTG
 GTNTTCAGAA AGTGGCAAGT TGGTAACTAA GATGTTCCAG AAGATTCANG
 ACTTGATTGA TGATAANNA NCTTTGGTGT TTGTCCTGAT TGATGANGTA
 AGCACTCANN GGTACTCATT CTTNGTCTGC ATTGCCTCTT GCTATTACTG
 CCTGATCCCT CTCATTGGT TCACTGTGTC GCNANCTCTT TTCTATGGAT
 CTTTTCCNNAN CCACCCGGTTT C

FIG. 6

PEGen 8-Rat phosphofructose kinase C

GTGACGTAGG GTCTGTTGCG TCAATGGTTA TAGCAAGTGA TGCTCTCTGA
 TTATTACTGC TGACAATACT CGGCCAACAA TTCTTGCATA GAGTGCTGAT
 AAATAACTAT GTTACAAAAAA GGGGTGGTCC CTGGAGAACAA TTACAGGCTT
 CCCTAGGTAA GTGTGCAGGT CAGGAGACGG CATATTCAAT CAGATGGCTG
 ATAGTTCTCC GTGGTTATGC ACCGGCTCCA GCTTGCCTAC GTCAC

FIG. 7

PEGen 13-Novel

GCAGCATGAT GAATTAAATG CAACAGTCAT AGCAGGGCAA GGGGAGAGAA
 AGGCAGATGG ACTATCTGCA TCATCAAGCG AGGGCTTGTG TCGGCGGCTA
 TGTGCAGAGA CGAGCAGGGC GAGGCACTTA AAAGCTGCTN GATGAAAATC
 CACCCAGGAG AAANTCTGGGC CTACGTCA

TGACGTAGGC CCAGACTTCT CCTGGGTGGA TTTTCATCCA GCAGCTTTA
 AGTGCCTCGC CCTGCTCGTC TCTGCACATA GCCGCCGACA CAAGCCCTCG
 CTTGATGATG CAGATAGTCC ATCTGCCTT CTCTCCCCCTT GCCCTGCTAT
 GACTGTTGCA TTAAATTCAAT CATGCTGCCA AAAAAAAAAAA A

FIG. 8

PEGen 14-Novel

GCCATAAATA CACTTTATT CATTGAAAT GCATAATCAC ACTGGGAGCA
 CTCCCTTGG AGCACTCCTC TAGCAGCAGG TCCGAAGTGC TCCAGCATCG
 TCAGCTGGCT CCAACACCTA CGTC

FIG. 9

PEGen 15-Novel

TTTTTTTTTT TTTGGAAACA GAATAAAAGTG CTTTATTCTC TGGCTGGCTC
 TCCTACGTCA C

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FIG. 10

PEGen 21-94% homology to mouse FIN 14

```

TCGGCGATAG CATTGGAGCA AGTCTTATCA GCAAGCAATG TTTTCAGTTA
TGTTCAAAG TTAAGAATGG GTTTAAACTT GCTGAACGTA AAGATTGACC
CTCAAGTCAC TGTAGCTTTA GTACTTGCTT ATTGTATTAG TTTANATGCT
AGCACCGCAT GTGCTCTGCA TATTCTGGTT TTATTAAGG AAAAAGTTGA
ACTGCAAAAAA AAAAAAA

```

FIG. 11

PEGen 24-Novel

```

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TNGCCAGGCT
ATGTCTCAGA CTTTATTATT ATTATTATTA TTATTATTAT TATAAATAAA
ACATGTNCTT TCAATTAGGT TACAANAGTA TTTATCTCCA TAACGCTTCT
TCATACATCC TTAGTTTGG ATTAAAGTAC CATCCACCCC AACTCAAAC
GTAACCCCCA GTAATCCCCT CTAACGTGGA AATTCTGGT TTAACAAC
AGTTAACTGC CCCACAAACA GTGGGAGGCC GCTCTGCAT GGCTATGCCA
CGTAACCCTT CACTGCTTCA CTTCTCGCT GGCT

```

FIG. 12

PEGen 26-Rat poly ADP-ribose polymerase.

```

GACCGCTTGT ACCATCCAAC TTGCTTTGTC TTCTGCAGAG AGGAGGCTAA
AGCCCTTGAG CTGGCTGGCA CTGTACTCAG GCCGGAAGCC CAGCTCGTCC
CGGTTCTTGA CAAAGCAAGT TGGATGGTAC AAGCGG

```

FIG. 13

PEGen 28-Novel

```

TGCCGAGCTG GGTATTGTGA CGGTTGATAA TGGCGGCATC ATGTTGCCAG
GTACCGGGTA AGCAGACCTC AGAGCACAGC TTATTGTCCA GTGCTTTCAC
GCTCGCGACG TCAAAGTCAT TGTTATTGTC ACACCTCCATG CCTAGAAATG
CGCATGTCCT CTGGCCATCT TCTTGCACAG GGGATCTGTC CTCTTCCTCC
ATGATATCAT TTCCCTCTGC ATCCTGCTCT CCAGCTGGAA GGCCAGCAAA
ATTGCTGTCT GGGGACTCTG CTGGGGTCTC CTCCTCTTCT GAAGGGGCC
TGCTAGCAGC TCGGCA

```

FIG. 14

PEGen 42-Novel

```

AGGGGTCTTG ATGGACTTGG GTCGGACATC TTAGTGACCT GTGAATTCTT
CTGTGGAGGC TGAGTCTCAC GTAGCCGAGT TTAATATCTG TGCTATTTAC
TAAAGTATCT GCCACCAAAT TGTACCAACT CATACTTTA TATGAATGTT
GATGAGTCTG TATCATAAAT AGAATTGTTG ATACATCCTT AATTTGTGCA
ATATTGTATG AAGAAGATTG TTATCAATTA AAACCACGCC TCTTTATGAT
CCTNNNAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
AACCNCCCTCA AATCCATNGG TTCTAACCCA AAACCCCT

```

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FIG. 15
PEGen 43-Novel

```
TTTTTTTTT CATAACCCAT CAAACCAATT TTATTTCTAT AGCAACGTTT
CTCACGTCTG AACCTGAGAA TAAGTCACCA GCTCTTGACA GTAAACATGG
GCCCTATCAA ATTATATTAG ACTCCTCAGT GTCCCGCCAT GTGGCCTTGC
ACCAAATCAA TTAGTTGAG GGCCAAAATC CTGTTGGGTT TCAAATAAAG
TGTCAAGGTCA TAAGGAGGGG GAGGGACTCA ATTCAATGGGA ACATTTTAC
CTGTTCAAAT AGATAAACTG AATTGCCCTA TCTGTGGTCA CCTGGATCCA
AGACCCT
```

FIG. 16
PEGen 44-Novel

```
CCCTGACGAT AAATGGTAAG GAACTTTTTT TTTTTTTTTT TTTTTTTTTT
TTTTTTTTNC GAAATAAACAA AACACAGCTT ATTATTTGGG GGAACATTAA
NTTCTATAAN TGAACACAAA ANAAAATTAA NANTTAATGG GGGGGTANAA
GGGACTTTGA ATCTATCTGG TATCATGACA TTGAAGCANA NACCTGANTG
ACCAGAAAGA GAGAGAGAGA GAGAGAGAGA GAGAGAGAGA GAGAGGTTTC
ATATGAGCTA GTGTTACAGG CTTTATTAGT CTATTAGTCA GGGACC
```

FIG. 17
PEGen 48-Novel

```
AATCGGGCTG GATGGGTGTA TCCGGCACTG TTTCGTAGCG GCAGCAACTG
GGTGCTTCTA TCTGAAAGCG GGCTTCACAA AAACACTACTGC GCCACCCGAC
TCGCTGCGGC ATCGCCCCGGT GGCAGTACCGT GTATCGCCTT TCCTGGTGCA
GAAGAAGTGT TTACAGGAGG CGGTCAATTAA CCGCAATCTG ATTCTGTTTT
TTATTCTCCC TGGCGGGTGA TCGCGATCGG CAGTTGAAA ACGATCGTTG
AATCCACGCT CGGGAAATGAT GTGGCTTCGC CGCCAACGCT TACTGACATT
TCATTGTAC AGCCCGATT
```

FIG. 18
PSGen 1-80% homology to *B. taurus* supervillin

```
GCCGAGCTGT GTAAAACCAT CTATCCTCTG GCAGATCTAC TTGCCAGGCC
ACTCCCAGGG GGGGTAGACC CTCTAAAGCT TGAGATTAT CTTACAGATG
AAGACTTCGA GTTTGCCTC GACATGACCA GAGATGAATT CAACGCCTG
CCCACCTGGA AGCAAATGAA CCTGAAGAAA GCGAAAGGCC TGTTCTGAGG
GTGAGATGAC AGCCACAGAG AGGTCACTGC CACTAGACCA GAAAGTGGAT
GGAGATATAT ATTTGGACTG GTGTTTTTTT CTGTCAG
```

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FIG. 19

PSGen 2-91% homology to human HTLV-1 Tax interacting protein

```

ATCGGGCTGC AGATTGGAGA CAAGATCATG CAGGTGAACG GCTGGGACAT
GACCATGGTC ACTCATGACC AGGCTCGGAA GCGGCTCACCC AAACGTTCGG
AGGAAGTGGT CCGCCTGCTG GTGACTCGGC AGTCTCTGCA GAAGGCCGTA
CAGCAGTCCA TGCTGTATA GCTGTAGTCA GCCTAGACTT CTGCCCACTG
ACCTTTTNGG GCACTGAGAA CACATCCACG CTCTGTCTGT ATCTAGTTCT
GGCTTCTGCT GTGTGCTANG CCCCAGCTCT GAGGAGTAAC AGCTGATCCC
AAAGGTCCAA GCCAACCTTC TTACCCCTCA GCCCCCCANCC CGAT

```

FIG. 20

PSGen 4-Rat proteasome activator

```

TTTTTTTTTT TTTGGGCAAC TATGTATTTA TTGTGTTTGG AAGGCAGAGT
GAGGGAGGAG ACCCCAGCAG GAAGAAAGACT GGGTGCAAGTC TAGAGTTCCCT
AGTCAAGAGT AGGAAGGTTT CTGTTATACC CATCATAGAA CGAGAGAGGG
GGCTCAATAG ATCATCCCCT TTGTCTCTCC ACGGGGCTTC TTGAGCTTCT
CAAAGTTCTT CAGGATGATG TCATATAACA CAGCATAAGC GTTACGGATC
TCCATGACCA TCAGCCGGAT CTCCTGGTAT TCCGCCTCGT CCAGCTCGGC

```

FIG. 21

PSGen 10-Rat Ferritin Heavy Chain

```

AANATCTGCT TAAAAGTTCT TTAATTTGTA CCATTTCTTC AAATAAAGAA
TTTTGGTACA AATTAAAGAA CTTTTAAGCA GATGTTTGG TGCAACTAAT
AGAAAAGATA AAGGCAGCCT GACATGCATG CACTGCCTCA GTGACCAAGTA
AAGTCACATG NCCTTGGGAC GTCAGCTTAG NTTTATCACN GTGTCCCAGG
GGTGCTTGTG AAAGAGATAT TCTGCCATGC CAGATTCAAGG GGCTCCCATC
TTGCGTAAGT TGGTCACGTG GTCACCCAGT TCTTTAATGG ATTTCACCTG
CTCATTCAAGG TAATGCGTCT CAATGAAGTC ACATAAAGTGG GGATCATTCT
TGTCACTAGC CAGTTGTGA AGTTCCAGTA GTGACTGATT CACACTCTTT
TCCAAGTGC A GTGCACACTC CATTGCATTC AGCCCCCTCT CCCAGTCATC
ACGGTCACNT A

```

FIG. 22

PSGen 12-Novel

```

TGACGTAGGG CCGAGAGCAA CAAGCACAGA ACTCCTTCTC CAGTTTCACC
CTGATGAAGT TGAGGCACTC TTCTGCAGT GGAGGGGCCA GCCTGGGGC
CAGGCACATT GGACACCACC TTCCCATGGA CTACAGCGTC AATGCCATTG
CCTTCTATTG CTATACCTTC TAGGGGCTGC CCCTCTTCCC ATTCAAGCCAA
CACTGAGTGT TGGGAGATTT CTCTTTTTA AAAACACATG AGAAAATAAA
TGCACCTTAC TCCCTCCCCA AAAAAAAA

```

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PSGen 13-Novel

GTAGGCAATA AAATGTTTC AGAGGTGCGA AAAAGCTTT GTTTCTTAA
ACCATTCTTA GTCTCTGCCA CACTTGACAC TCCGTCAAAG TGAGAACGGA
ACTAAAGACC AACTGCGGTG GAAAATATTA TGTTTATGTA ATAAAAAAA
ATCATGTAAC TGCAAAAAAA AAAAAAA

FIG. 24

PSGen 23-Novel

TGCCGAGCTG AAAACATACA TCCGCACCGG GTTGAGATAG CTGGCCCTCC
GTCCCCGGGC ATACTCTTG GATAAGAACCC CGGGCCTTGT TACCAAGGTAC
CGGAGTGAGC TGAAAAATT ACCGTCGAAA TGGGTGATGT CCTGGAAAAA
ATGGTTCAAC AGCTGCCAGG CAGATTCTT GGGTTCCACA TTTTCCTGCC
CACAGATGTG GCAGAACGCG TCAAGTAATG CAGCATTACA ATTGAGGCAG
ATCTTTCTT TTCTTCCTT GGAGTGGCTC AACCAAGCGAT TTTGGTTAAA
AATAATCAAA AAAGCGACGG CAAAACTTT GTTATATTCC CGCCTGTGGC
ATTTGAAC TGCCCCGGCAA CCGAATAACT TTTAATTTCG AAAATAAAAT
GCATACTAGA TTTTAGCGG TTGCCTCTG GCCATTGCTT CAGGCGCCNG
CACAGCGTCA GCCCAGTTT ACCACNANGA ATATCCTAAG CGTTGAAACA
GGGCACAGCC GAAAAAAACN CTGGCNACAA AAAANATCCG GACATCCTT
TTCCAATTTC GAAACCGAAN GCNCGCAAAC NAAGGTTCTT CGGGAAAAAA
AATCGCCAAA ATACNCGANA TCAAACNTNC CAA

FIG. 25

PSGen 24-Novel

TGCCGAGCTG GGGGGAGTTC CAGGAATTTG TGGACTATTT CCAGGAGGAA
TTGAGGAATC TAGAAGTAAT AAGAACTTCA CAAGTAGAAC AACAGAGTTA
ATTGACCTCT ATCCTTAAGA GTTACCAAGAG AATTATTAAA AAACTAAAGA
ACAATCAAAG CCTGGTCCTG TGCCACCACC CAAAAACATG TATAGCCTAT
GTGCAGCTCG GCA

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FIG. 26

PSGen 25-Novel

CTCANAGGGC NNNTTNGNGG NCNTCATGCN CCAGGGNTCCN NCCCCCANAN
 GANCNNCCNG GTAAACTACA CNGGAGTACT TAAGTGGACA NNCCACATGC
 GANGGNCAAG GGGATCACCN TCNCTCCTNC AGNCTTNCG TGNCTCTCCT
 GTNCNTNCAC TGCCNCANAA NGGANGCNCN NNCTCCTATC TGTNTACAGN
 AACACNTNGCN CTNNCTCTAA GCTCNCCCAC TNTGTGGAAA GGCAATGTGT
 GCGTGCCTCT CCCCTATCAC GGCGNGTTGC NAAANGGGGA TGTNCTGCNC
 GGCGATGAAG TTNGGTCACT CCATGTTCC CAGTCCNACC TGTTAGACNA
 AGNATTGNAN TGTGATACGA CTCNCTGTAA GGGGANTNGC GGACCCAGTA
 TGTTTGGCCC NACNNCCACT TCTTTAAATG GTGGCTAACG GCGCTTCCTA
 GNATAAACAC TATTGGTCCC CCCCTCTGCA GNACCCNTTA CTTCCGNANA
 AAAATTGTTG TCNTGATCCG CGACAACCAC ACCGTCTGTN GNTTTTAGTT
 GCAACNCNNA TCNCTCCAAA AAAGTTTCAG AAATCTTCAT TTTCCNGGT
 TGAGCCCNtg ACAAAACCCCT NAGGATTGT CGAATGTAAA GTCTCCNGAT
 CTTCAATAAA NNTCCAAAAG NCTANCGAT

FIG. 27

PSGen 26-Novel

TCACTGGCN NNNTGGTNGN CGTCATGCNN NAGGTTCCNN CCCCCNNANG
 AACCTCCNGG TAATCTACAC NGGAGTCTTA AGTNGACAAN CCCACACTGC
 GANGGTCAAG NGGATCACCA TCNCCNCCTC CCAAGCTTNT NCATTGATGC
 TCTCTCTGTT CCGTNCCCTG CCGCTACACA TGGANGCTCT TNCTCCTTNT
 CTCNTCTTAC NANNCAAACA TTGCCCTNTC TCATA

FIG. 28

PSGen 27-Novel

GGGAANGGGA NNAAAAGGA ATTTTTNGG GGGGGGNTTN TCTGGGAAAN
 TTTTTTTTT TTTTGGNAA AAANGGGGGG GGAAANAANC CGNTTTCCC
 NAAAACNGGG GGGAACNGGC CGGGGGGGGA AAAAAAAGGG TTACNAAGGG
 AACACTTNA AANNGGAANG GNTTGCNNC CCTNTNGAAA NNTTGCCCC
 CCNNNAGGAA TCCCNNGNNA AACCCAANN CNNCNCNCNG GGGNCNNNTN
 CNANGGGACC CCAACNCGGG CCCNAACTNG GGGNAAANAN GGGCAAAACN
 GGTNCCCGGG GNAAAANGGT ANCCCCCTC

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FIG. 29**PSGen 28-Novel**

TGCCGAGCTG GGGGTGAAGC ACCGGAAAAC AACCGATCCA TCTCTTATCA
 CAGGGTCTCC AAGATCCAA ACCCAAAAGC CACATTGTTA ATTAGCCTTT
 TTATTGTGTT TTTTTTTTT TTTTTTTTT TTTTTTTTT TTTTTTTTT
 TTTTTTTTT TTTTTTTTT TTTTGGCAGC TCGGCA

FIG. 30**PSGen 29-Novel**

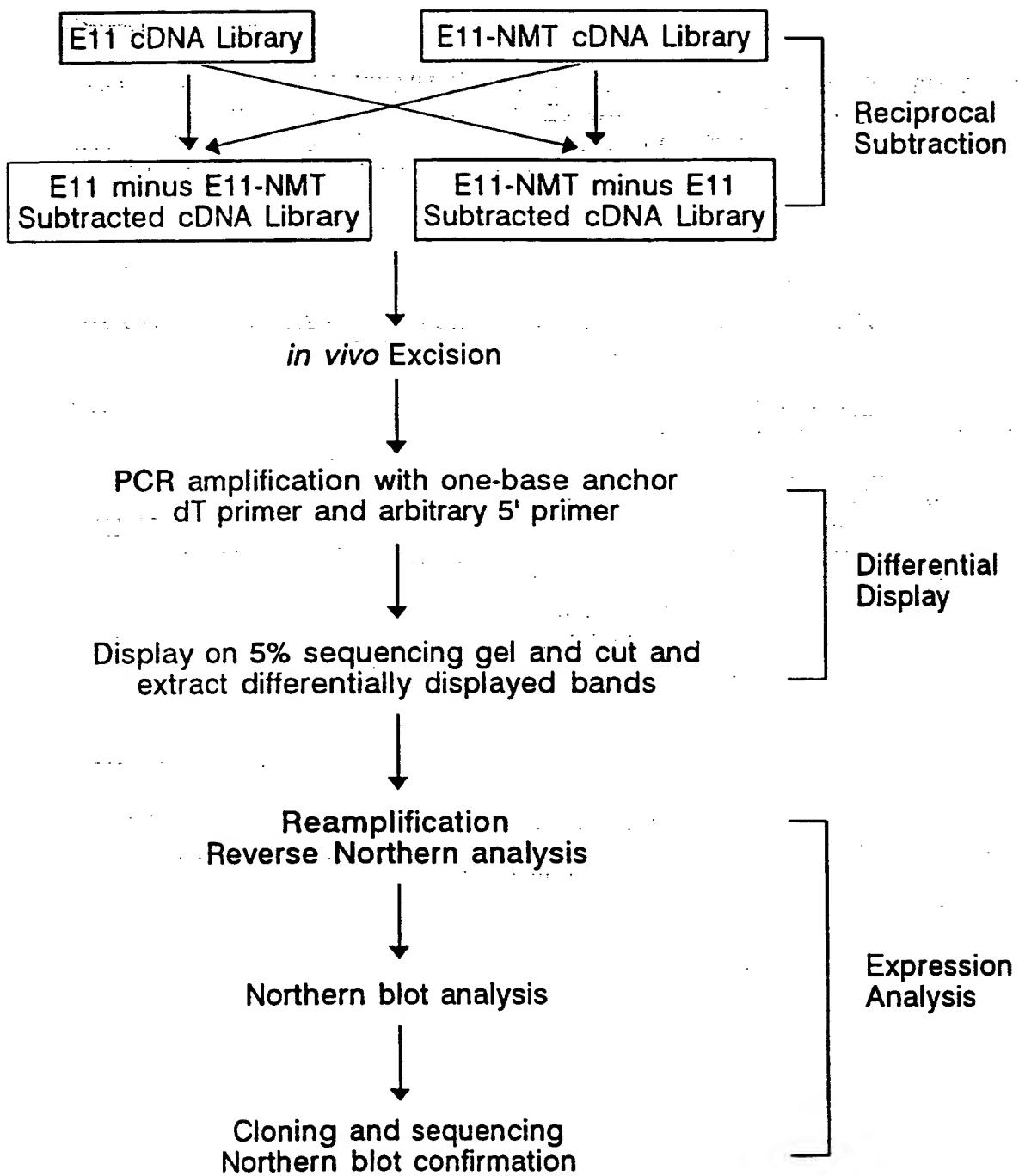
TACGGGCGCT GATTTTACG AACATTACCT GGCAGGGAAA TTTGATAAGT
 ATCCACTGTG GGTGGCGCAC TACCTGGTAA AAGACAAACC CCGTGTGAAA
 AGGCCCTGGA CTTTTGGCA ACACAACGAA ACCGGCCACG TGAATGGCAT
 CCGGTCTTAT GTGGACTTCA ATGTTTCAA CGGGGACAGC ACAGATTTG
 CCGAACTATT AATGAAATAA TGCAGAATT CGCTTTCAA ATAAGCCCAT
 GGATCCTGAC GTAAAATATT TCCTGCTGGT GATCGTGCAG TCCATTCGA
 TGCTCATACT TTGGCTGATG CTCAACATGA CCTTGAGGAT CTATTTAAT
 TTTGCTTTCC CCGACAAATGG TTTGACGCTT GGCAACATCA TTTATTACCT
 CTTCTGCTG GGCAGCTCGG CA

FIG. 31**PEGen 32-Novel**

TNCATANGCC CTGAGGTGGG GACGAAGCCC GAGTCCGTCC TGACATGTTT
 CCAGTGGAAA AGATTTGTT NTGAGCGTTN CTTTCTNNNT TNTTTNNNT
 TGNTTGTNN ATGTTTTGT TGTTGTTTN TTNAAACTGT NTGTTGNCAN
 TTCAACATNA ANGGNAGGNA ANTNTGTGNC TNCNTTGCAN TGTNNCATGN
 TNCCCANANC CAAAAAAA AAAAAAAA AAAAAGAGTA CAAATATCAC
 AAAATTTGAC ATTTTGTAA TAATACTTTG GTTGTGTTT GGTGACGGCG
 ATTG

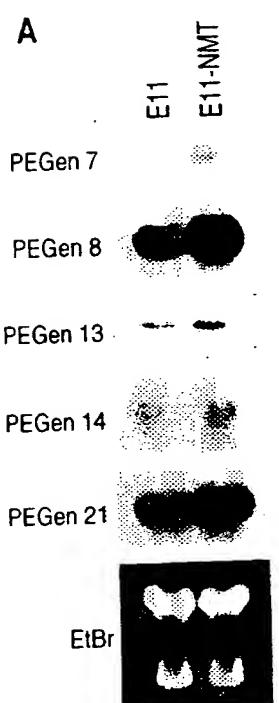
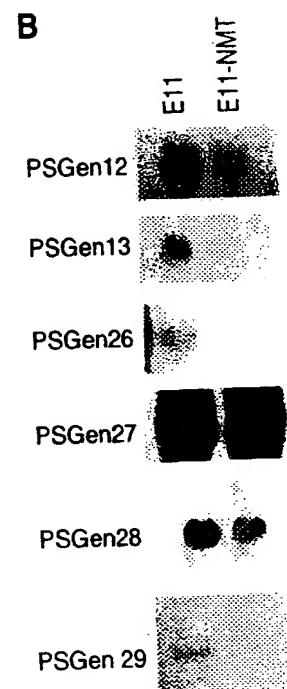
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FIG. 32

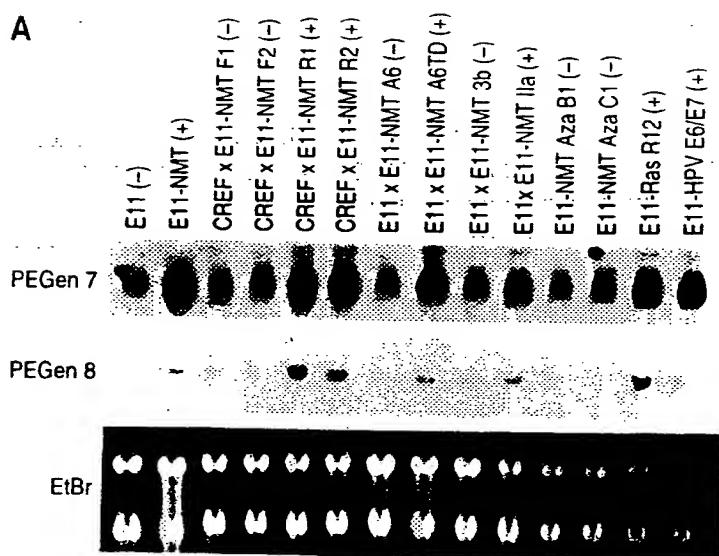
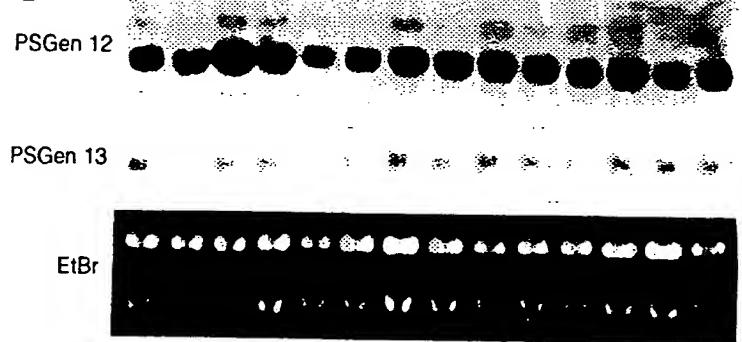


SUBSTITUTE SHEET (RULE 26)

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FIG. 33A**FIG. 33B**

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FIG. 34A A**FIG. 34B B****SUBSTITUTE SHEET (RULE 26)**

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FIG. 35A**PSGEn 12 cDNA Sequence**

GGGGTGGTGA CGGTAGTATG GCCGCACTTT ATGGTGGCGT GGAAGGGGGA
GGCACACGGT CCAAAGTCCT TTTACTTTCT GAGGATGGGC AGATCCTGGC
AGAACGAGAT GGACTGAGCA CAAATCACTG GCTGATTGGC ACAGGTACCT
GTGTGGAGAG GATCAATGAG ATGGTGGACA GGGCTAAACG GAAGGCTGGA
GTGGATCCTC TGGTACCCCT TCGAAGCCTG GGCTTGTCCC TGAGTGGTGG
GGAGCAGGAG GATGCAGTGA GGCTCCTGAT GGAGGAGTTG AGGGACCGAT
TTCCCTACCT GAGTGAAAGT TACTTCATCA CCACTGATGC AGCAGGTTCC
ATCGCCACAG CTACACCGGA TGGTGGGATT GTGCTCATCT CTGGAACAGG
CTCCAACGTG AGGCTTATCA ACCCTGATGG CTCTGAGAGT GGCTGTGGTG
GCTGGGGCCA CATGATGGGA GACGAGGGAT CAGCCTACTG GATTGCACAC
CAAGCTGTGA AAATTGTGTT TGACTCCATT GACAACCTGG AAGCAGCTCC
TCATGATATT GGCCATGTCA AGCAGGCCAT GTTCAACTAC TTCCAGGTGC
CAGATCGGCT AGGAATCCTC ACTCACTTGT ATAGGGACTT TGATAAGTCC
AAGTTTGCTG GATTTTGTCA GAAAATTGCA GAAGGTGCAC AGCAGGGAGA
CCCTCTTCC AGGTTCATCT TCAGAAAGGC TGGGGAGATG CTGGGCAGAC
ACGTTGTGGC AGTATTGCCA GAGATTGACC CAGTTTGTT CCAAGGGGAG
CTTGGCCTCC CCATTCTGTG TGTGGGTCA GTGTGGAAGA GCTGGGAGCT
ACTGAAGGAA GGCTTCTCC TGGCACTGAC GCAGGGCCGA GAGCAACAGG
CACAGAACTC CTTCTCCAGT TTCACCCCTGA TGAAGTTGAG GCACTCTTCT
GCACTGGGAG GGGCCAGCCT GGGGGCCAGG CACATTGGAC ACCACCTTCC
CATGGACTAC AGCGTCAATG CCATTGCCCT CTATTCTTAC ACCTTCTAGG
GGCTGCCCT CTTCCCATTG AGCCAACACT GAGTGTGTTGGG AGATTCTCT
TTTTAAAAAA CACATGAGAA AATAAATGCA CTTTACTCCC TCCCCAAAAAA
AAAAAAAAAA AAAAAAAAAA AAAA

PSGEn 12 Protein Sequence

GGDGSMALY GGVEGGGTRS KVLLSEDGQ ILAEADGLST NHWLIGTGTC
VERINEMVDR AKRKAGVDPL VPLRSLGLSL SGGEQEDAVR LLMEELRDRF
PYLSESYFIT TDAAGSIATA TPDGGIVLIS GTGSNCRLIN PDGSESGCGG
WGHMMGDEGS AYWIAHQAVK IVFDSIDNLE AAPHDIGHVK QAMFNYFQVP
DRLGILTHLY RFDKSKFAG FCQKIAEGAQ QGDPLSRFIF RKAGEMLGRH
VVAVLPEIDP VLFQGELGLP ILCVGSVWKS WELLKEGFLL ALTQGREQQA
QNSFSSFTLM KLRHSSALGG ASLGARHIGH HLPMDYSVNA IAFYSYTF

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FIG. 35B**PSGen 13 cDNA Sequence**

GGCACGAGCT CTCCTCGTCC CCTCCCTTCT CCAC TGCAGC CTTTCTCTTA
GCCCGAACCA CTTCCTTCTT CTGCTTGTTC CTCCCCTAGGG CGCGGAAGCT
GAGTGCAGGG TTCAGACCCA CGCGCGAGC AGCTCTTCAG TGAAGAAGGA
AGCAATCGGA GGGTCAGCAA TGAACGTGGA GCATGAGGTT AACCTCCTGG
TGGAGGAAAT TCATCGTCTG GGTTCCAAAATG GCCGATGG GAAACTGAGT
GTGAAGTTTG GGGTCCTCTT CCAAGACGAC AGATGTGCCA ATCTCTTGA
AACCGTTGGT GGGAACTCTG AAAGCCCCGCA AAACGAAGGA AGATTGTTAC
GTACGCAGAA GAGCTGCTTT TGCAAGGTGT TCATGATGAT GTTGACATTG
TATTGCTGCA AGATTAATGT GGTTGCAGA TCTGGGGGTA TCTGGTAAAC
TGGAAATAATT AAGTTAAAGG ACAAACATGA AGTTCTTAT GTATTTTAT
AGACCTTTGT AAACAAAAGG GGACTTGTG AGAAGTCCTG TTTTTATACC
TTGGAGCAAA ACATTACAAT GTAAAAATAA ACAAAACCTG TTATTTTTT
TTTCTTAAGA AGGTAATCGG GAGACGTAGG CAATAAAATG TTTTCAGAGG
TGGCAAAAAG CTTTGTTT CTTAAACCAT TCTTAGTCTC TGCCACACTT
GACACTCCGT CAAAGTGAGA AGCGAACTAA AGACCAAATG CGGTGGAAAA
TATTATGTTT ATGTAATAAA AAAAATCAT GTAAAAAAAAA AAAAAAAA

PSGen 13 Protein Sequence

MNVEHEVNLL VEEIHRLGSK NADGKLSVKF GVLFQDDRCA NLFETVGGNS
ESPQNEGRLL RTQKSCFCKV FMMMLTLYCC KINVVCRSGG IW.

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FIG. 35C**PEGen 28 cDNA Sequence**

GTGTGGTGTG TCTCTCAGAC GTCCGTGACA CTTGATCCT GCCCTGCCGG
 CACCTGTGCC TCTGCAACAC CTGTGCAGAC ACCCTGCGCT ACCAGGCCAA
 CAACTGCCCG ATCTGCCGGC TGCCCTTCCG GGCACTGCTT CAGATCCGAG
 CCATGAGGAA AAAATTGGGC CCTCTGTCTC CAAGCAGCTT TAACCCCATC
 ATCTCTTCCC AGACTTCGGA CTCTGAGGAA CATTCATCCT CAGAGAACAT
 CCCTGCGGGC TATGAAGTGG TGTCTCTCCT GGAGGCCCTC AATGGGCCCC
 TCACCTCATC CCCAGCGGTG CCTCCCCCTTC ACGTTCTTGG AGATGGCAC
 CTCTCAGGAA TGCTGCCGTC CTATGGCAGT GATGGCCACC TGCCCCCTGT
 TAGGACACTG TCCCCCCTTG ACCACCTGTC TGATTGCAAC AGCCAAGGGC
 TCAAACCTCAA CAAGTCTCTC TCCAAGTCCA TTTCCAGAA TTCTTCTGTG
 CTTCACGAAG AGGAAGATGA GCGCTCTTGC AGTGAGTCAG ACACTCAGCT
 CTCTCAGAGG CTGTCAGCCC AGCATTCTGA AGAGGGACCT GATGTGACTC
 CAGAGAGTGA GAACCTCACG CTGTCCTCCT CAGGGGCTGT TGACCAGTCA
 TNTTGACAG GGACTCCGCT CTCTTCCACC ATCTCCTCCC CAGAAGACCC
 AGCCAGCAGC AGCCTGGCCC AGTCAGTCAT GTCCATGGCC TCCTCCCAGA
 TCAGCACTGA CACCGTGTCC TCCATGTCTG GCTCCTACAT TGACACCTGGC
 ACAGAAGAAG AAGGAGAGGC CCCACCTTCC CCCCAGCTG CTAGCAGGGC
 CCCTTCAGAA GAGGAGGAGA CCCCAGCAGA GTCCCCAGAC AGCAATTGG
 CTGGCCTTCC AGCTGGAGAG CAGGATGCAAG AGGGAAATGA TATCATGGAG
 GAAGAGGACA GATCCCTGT GCAAGAAGAT GGCCAGAGGA CATGCGCATT
 TCTAGGCATG GAGTGTGACA ATAACAATGA CTTGACGTC GCGAGCGTGA
 AACGACTGGA CAATAAGCTG TGCTCTGAGG TCTGCTTACCG CGGTACCTGG
 CAACATGATG CCGCCATTAT CAACCGTCAC AATACCCAGC GCCGGCGACT
 ATCACCCAGC AGCCTGGAGG ACCCTGAGGA GGACAGGCCT TGCGTATGGG
 ATCCTTGGC TGCTGAGGG CACTGGCACC TGTACCTGGG CTTCCCTC
 TGTCCGCCCTT CCATCTGTCC TCACTGGACC ACAGGCCTTC TGGGCATCTT
 CAACAAGACA CGTGGACTTT CTACTCTCAT GAAGGGAGGA CAGTGAACCC
 CTCCACCAAC TTCATCTCCT GTAACCATGA TTCTTACCCCT CTCAGAAAGT
 ACCAGAAGCC TTCCTCCTGT GGGCTGATGT GTGCCAGCCA AACCCAGTGG
 GTCAGCTGAG CTGAGGGTCA GGGCTGGTTG TTTCTGTAGC CTTTCTCTT
 CCAAATGGAG ACCAACGAGA AAAAAAAA AAAAAAAA

PEGen 28 Protein Sequence

VVCLSDVRDT LILPCRHLCL CNTCADTLRY QANNCPICRL PFRALLQIRA
 MRKKLGPLSP SSFNPPISSQ TSDSEEHSSS ENIPAGYEVV SLLEALNGPL
 TSSPAVPPLH VLGDGHLSGM LPSYGSMDHL PPVRTLSPLD HLSDCNSQGL
 KLNKSLSKSI SQNSSVLHEE EDERSCSESD TQLSQRLSAQ HPEEGPDVTP
 ESENLTLSSS GAVDQSXCTG TPLSSTISSL EDPAASSLAQ SVMSMASSQI
 STDTVSSMSG SYIAPGTEEE GEAPPSPRAA SRAPSEEET PAESPDSNFA
 GLPAGEQDAE GNDIMEEDR SPVQEDGQRT CAFLGMECDN NNDFDVASVK
 ALDNKLCEV CLPGTWQHDA AIINRHNTQR RRLSPSSLED PEEDRPCVWD
 PLAV.

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FIG. 35D**PEGen 32 cDNA Sequence**

GGCACGAGGC GCCGCCTTCC TGCTCGCGCC CTATGCCGC CTTCCGTGCTC
GCGCCCTATC GCCGCCTCCG AGTCCTCCTG CGCCCCGGGC TTCCGCCGCT
TCATTGATT CCCTTCTCG CCGCTGCAGC CTCCTGACAC GGTGATCCGG
GCGGGCCCCG CAGGAATTTC ATCCCCTCAC CGGCCTCACA CTAGTGTGCG
ATGTCCACTA TCCAGAACCT CCAATCTTC GACCCCTTTG CTGATGCAAC
TAAGGGCGAC GACTTACTCC CGGCAGGGAC TGAGGACTAC ATTCAATAA
GAATCCAGCA GCGGAACGGC AGGAAGACGC TGACCACTGT GCAGGGCATT
GCGGACGATT ATGACAAAAAA GAAACTTGTG AAAGCTTCA AAAAGAAATT
CGCCTGTAAT GGGACTGTGA TTGAACACCC TGAGTACGGA GAGGTCAATT
AGCTTCAAGG CGACCAAAGG AAGAACATT GCCAGTTCT TTTGGAGGTT
GGCATCGTCA AGGAGGGAGCA GCTGAAGGTT CACGGATTCT AAGATGAACC
CGAACATGTG GCGAGTTCT TAAAATGGTTT TGTTGTCTAA CTCAGTTGG
CTGCCTCGGG AGATGATTCT TTACAGTAAA CGACAGACTT TGC GTTATT
AAATCATTCA GACTTCCACT CACGCCTGCA TGGCTACAGA AAACATGGGG
TATGTAGGCT CCTAAGTCAC AAGGAAATCG CCGTGAGGTG GGGACGAAGC
CCGAGTCCGT CCTGACATGT TTCCAGTGGA AAAGATTTG TTCTGAGCGT
TCATTTCTAG TTTATTTCA CTTGATTGTT AAATGTTTTT GTTGTGTTT
TATTAACCA TGTATGTTGC AGCTTAACAA TAAAGGAGGA AAGTCTGTGC
GTCAAAAAAA AAAAAAAA AA

PEGen 32 Protein Sequence

MSTIQNLQSF DPFADATKGD DLLPAGTEDY IHIRIQQRNG RKTLLTVQGI
ADDYDKKKLV KAFKKKFACN GTVIEHPEYG EVIQLQGDQR KNICQFLLEV
GIVKEEQLKV HGF.

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FIG. 35E**PEGen 42 cDNA Sequence**

GGC GTT GCGA CGT GGACATG TCG GC GT CGT TGG TCC CGC GC CAC CGT GC CGG
 GCC GTG AGCA AGAG AAA ACT GCA ACC CAC G CGGG CGG CGC TCAC GCT GAC
 CCC CT CT GCT GTG AACA AGA TAAA ACA ACT TCT TAA AGAC AAG CCT GAG C
 AT GTG GGG TCT GAA AGT GGG GT GTG CGG ACCA GGG GCT GT TAA CGG CCT CT C T
 TAC AGC CT GG AGT ATAC AAA GAC AAA AGGA GAT GCT GAT G AAG AAG TTAT
 TCAAG AC CG GA GT CC GAG TGT TCAT CGAG AA GAA AG CCC AG CTA ACC CT GT
 TAGG CAC AGA GAT GG ACT AT GTG GA AGA CA AACT GT CC AG TGAG TT GTG
 TTCA AC AA CC CCA AC ATCAA GGG AAC CT GT GG CTG CGG GT AA AGC TT TAA
 CGT CTG AAG AG CT GAG GACT G CAA ACT CC AG GAG AG CT GG TCT GG
 AGC AC ACC GA AG AA AT CAT G TGAT GT CC CG TG CGG AAG T TAG GT GT GG
 CTG C CT CG TG GTG AGA ATA AAG TGA AGCA TTG AAA ATCA AGC CAG CGT G
 TTAG AGT TCC AAA AAC ATGG TGT CT GT TCT GT TGT AAG AGCA CAA AT GG AGA
 GAAC AT GG TG TCT GTT CT GGAGG AC AC AACT GAG AAA CT GT GAG TC
 CT CT GT CT G TAC AG AAA AC TC CT ACC CT G CC CT TAC G CT GT AG CT G CT
 CT GT G CT AGA ACC AG CT TC G TG ACC ATT G C TT G CT GG G A ATT GAG G AAT
 GGG ATA AC GG GT GT G C AC CT GGG T CAC AGA AT GG CT TG AG ACT GT CT C CT
 GG CC CT GT CT CAC CT CAG GC AGG CAG CT G TG GG AGC AGC AG CT GT GG G A
 GCG GT GAG GG GAC CT GG TT CC CT CAC CT G TG GG GT GG C CG TT G C AT CT
 TT ACC AC GT TG CCT GTT GT CA GAT AC CT CAT TT G CC AGC CT CC AG CA AG CT
 CAG CT AT GAG TG CC AGT CT C AGG AGG TAG G AT CAC CGG G CT GG GT CAG
 TCT GT C CT CT GGG CGT GCT TC AT GCG GT TT TG CT TAG ACC TTT CAG T TAG
 AAG CG CTT GT GAT GAG CAG CAG GT AG ACC TG CT GAG AGC GT GG TT CT CA
 GAG CT T CT G CC AG CC CT CC TC AC AGG TCA CAG CAG AC AG TG CT GT CT GA
 GAC ACT CG GT GAG GAG AC AT CCT G CT GG CAG T GCT CT T ACC AGT TT AG
 AG ACT G CATT AG TTT CT CT TGA AT GGA AG CCT GT GT AA ACC CTT TT GT
 CT GAA TGG CC AT CCT GTT TA GAG CTT GAA CC AG T AG T GT CTT CAG
 AAG AT CT GCA GC AG AG GG GT CC CT CAG AC GG CAC CT G GGG G CAG AA
 CAT G CAC ACA CTT AC AGT TG CC AGG GT GCA GAT GCT CC CT GCT CCC AGA
 GGA AG CT T CT AAG TTT CT TT AAT GT GG TCA TC ACC AGT TT TTT GAG CC AT
 GG TTT GCT G TATA CT AC AG GC CAG C CT TG AAC CC AC AA AC AT CCT CT G
 CTT CC AC GT T CAG AGG CAT G TG CT ACC ACA CCT GAC CT GG AT CCT AAG TT
 TCT CT TA AG TGG CT TG AT GG ACT TGG GT CGG AC AT CT TT AG T GAC CT GT
 GA ATT CT CT GT GG AGG CT G AGT CT CAC GT AG CC GAG T TT AAT AT CT GT G
 CT AT TT ACT A AAG T AT CT GC CAC CAA ATT G TAC CA ACT CA TAG TTT TATA
 TGA AT GT TG A TG AGT CT GT A TC AT AA AT AG AAT T GT TG AT AC AT CCT TAA
 TTT GT GCA AT ATT GT AT GAA GA AG AT GT TT AT CA AT TA AA ACC AC G C CT C
 TT AT GAT CC TAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA
 AAAAAA

PEGen 42 Protein Sequence

RCDV DMSA SL VRAT VRAV SK RKL QPTRA AL TLTP SAVN KI KQLL KDK PEH
 VGLK VGV RTR GCN GLS YTK TK GD ADE EVI QD GVR VF IEKKA QLT LL
 GTE MDY VED K LSSE FVF NNP NIK GT CGC GE SF NV .

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FIG. 3F**PEGen 45 cDNA Sequence**

ACGAGCTGAA GGTCACTTCG CGCACGGTT GGACCTGGGG CAGGTTGGAG
GAGTAGGAGT ATGTCATTGG GCGCGAAGAC GGGGCTGGG GCAAAAAAGA
AGGGAGGCTG GAGAAATCTG GACCCGAGAC GTAGTAAGTA CAACTTGGCA
AATAACATGTT AGAGGAGCAG GGACCACGCT CATCAAAATC CATCATGGG
CTACCTTGGG CTCTCCGCAG TAGCCGAGCT TAACATGATT CTCCACTGCA
GCTGCCTCTT TGAAGCGGAT CCGTGAAGTA GAAATTGGA GACGTAAGCT
GACGTGGAAA TCTATCCCCA TCCTTAGCAG GGAGGTGCTG GTCATGTGAC
CCGATGTTGA AATTGACAAG CCGCGAGCTA GTCCCCGGCTT TTTTTTTTA
ACCCCCCTCC CTTTCCCTTT TTCCCCCTCC CCTCCCTCCT CGGCTTCCTT
TCTTTGTAGC CACCTCAGGG GAAGCAACAG ATCGTCACTC GGTGTTCTCA
CCGAAAGCAC GTAATCGCCG GTGTAACTCA TGTTGGCTGG GGGGCCTCCC
CGCTCGCAGA AAGGCTGGGG TGCGCCCCCA AGCAGCTTC CTTTGCTCAG
CTGCATGGTC CTGGTCCACG AGCGCTCTGA GGGCGGCAAG AGAGCGAAC
TCCCTGACGCC TCCCCCCCAC TCCCCGGTGGG TGAGGGATGC TCTGGGATGG
GGGTGGCCAG GTGAACGCC C GGAATTGTGT AGCTTCAGGT TCCGGAGTCT
GTTGTCCGAA GGCTTACGTT CAGCACCTC TTCGCAGTCC CCCTCCACCA
GACTTGCTCT GGAAAGCACC TCAGTCTCAG AATCTGGCTG GACCCCATTT
GGGGCCAGGC TTCGCAGCCA CGATGTGCCG GGCTTCGTGG CTTGTCCGAT
TTGCACGGTG ACTTGATTAC ACGCTCTCAT TCATGGTCAC TTCCGAAGCG
CTTTAGTGCC TTCCGTCCCC AAACCGCCAA CAGGCAAAGC GGCTTCCCTC
CGCGGTTTGT CAATAATCCG CGCTGTCCGG AAGGGCTTCG CCTTACCCGG
GTTCCACCTT CCCTGTATCT TTCTGCTTAC TTCCTCATCC CACACTCTGT
CCTTGGAGGA ACCCCTTCTC CTCGCTGCCT GTAGGGGTTT GCAGTGACTC
CACAGAGCCA GAGGCGCTTC TGCTCACCGG TCCGCAAGCT GCCTGGTCTG
CTGAAGCTGA CGAATCGGGA AACCATGCAA TTGAGGCAGA CCTTGGGCTG
CTTTAGAGGC GCTGAGGGAGC CTTCTCCTGG GAGGCCAAG GTCGATTTC
GCCCAACCAGG ATCTGGGAA GACCCAACA GGGGTAAGAG CACACCGGAA
GGCCAAGTCC GAGTTCCAGT CCTAGAAGAG GCGGCTGCAG GCAAGGTTAT
GACATTGGCC CTGGACACTG GTTCCCAGG AGCTATTCTT TCTCAAGAAC
TCCACAGCAC GGGGCTGTCT CCAGAAAATA CTCTTCAACG TTTATTCCT
TTAATCGTCA ACCCGCAGCC CTACGGCGGT TAATGCGAGA GGCAAAAAT
GTTTGGAGGA AGAAAAACAA AGGCAGGAAG TGGCCGCGGC CTGACGGTGC
GTGTGTGTCT GTAAAGAAGG GAGGGAGCCG GTTCAATCTC TTCTTTTTT
CCCCGAATT CAAGGTTAG GCAGACCCCC GTAGGGCCTG GCCGAGGCTC
ACCCGGCGGA GCATTTGGAG GTGCCAATG AGTAAGGCTC GTCGGGCTGA
AAGGCTAAGA AGGAGATTG ATCGGCAGAA CAAACCAAGC CTTTTGGAG
GTTTCTTCTG ATTGGTCCT AAAGGGTATA TGCTAGTGTG CACAGCGGCT
CCTGTGGCTG CTGTTTCCCT CCTGTCGGAC TAAATGTACC AAGAAGGGAG
AGAGATTGAG GCACCTTGGC CGCTCCTCTC TCCTTCCGAG GTAGAATATC
AGAATAAAAGT GTATTCAAGGT GCCAA

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FIG. 35G-1**PEGen 50 cDNA Sequence****A:**

ATCGGGCTGT ACTAACAGAT TGTTTGTAAA CAGTGACACA GTGATAACTT
CCGTGTTACT TCTTAACTT ATGTTTCTGC TTTCAGATCT CCCCTCCCCTT
CCAGAGGAAG TTAGCGATGC CATAGCTTTA ATGTCTGTT TAGCTGCAAA
ACTCATTGTT CACTTCGT TAGAAAATCT AAAGCAGGTG GTATGCAATT
TCTCTTGATT TGGAATTCTT TAAAGGCAAG TAAATTTGGA ACTCCTGTGT
TGGGGGGTTA ACGGAGGTAG GAACCCAATG GTGTGTCCCT AGGTCGTCCC
CGTTCTCGGA TAGCACAGTC TGCATAGCCA TAGCTCTCAA TTATGTCACT
ACCCTAATCA TCGCAGCCCG GTCTCACCG ACTCTTGAA GTCCCAAAT
GACTTTGTT TGATCCTGAT TTGGATTTTC AATGGAAAGT AAAAGCTTGG
GGTGAGGAAG CAGCAGCTAA ACCAGGGAGT TGAGCCAGTG AATTGCTGAC
GGAAAGGATT CTGGTCTTGG AGGAGGGGGA CCTGAAGCAG AAGGAAAAGG
GATCCTTCGC TTAAGTTCTT AGGAAAAATC TTGACTCAGA ATCCCAAGAT
TTTCCCTTC ATCCCAGCCG GGTAAATATT TGGTTTGTC TTTTAAGTAT
AGCATGAAGC CGTGGATGA GAGCCATGTG TTGTAGGATT CTCTCCCTA
TTGGCTCTGA GCTTGTGTCA CCGTATCAGT TTGCTCCCTA CAAAGGGACC
TAGTTTGGAA AGGATTGGAA GGGCAACTGT TCAGCGGCAA TGGAACACCC
AAACGTGGAC TGGGACAACG GGATTCTGAT AAAGGGAAAT TTCTGGTCTG
GTCCTGGCTG TGTCTAGCT CTTTATGTGT GCATGGAGAG CTCTTGATCC
AAGTAGAATA TGTAACAATA CAGACCAGGA TCTTCCAGTC AGTACTGCTG
GGTGGAAAGTG GGCAGGTGAT GGTAGTTGCT AGAAGAATCA TTAAGACAGC
ATCTGCGGTG AATGCGTCCC AAAGCCTCGC GGCATCAGTT TCATCTCTAA
ACCATTAGCT TACAGTTGAT TCCGTTTCCT GGGACAGAGA AACATCCCCA
CGCGAAGTGA CTGTGTTGTG TATTCTAGC ACTGCAAATA AATTACCGCG
CCATGATGAA ACCTTGCAAA TACGCTTGAA CCAAAAAAAA AAAAAA

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FIG. 35G-2**B:**

GGGTGTGGGG CAGCTGGGTG GGAGCAGCGT GCAGGCTACC AGCACCAAGT
 GGTGTGCCCTC TCCGGGGGTG TGTGCAGAAG GCTCCTGGGG AAAACTGCAC
 AGGTACCAACC CCTAGACAGA AATCGAAAAC CCACTTCTCT CGGTGCCCCA
 AGCAATAACAA GCATTACTGC ATCCATGGGA GATGCCGCTT CGTGATGGAC
 GAACAAACTC CCTCCTGCAT CTGTGAGATA GGCTACTTTG GGGCCCGGTG
 TGAGCAGGTG GACCTGTTT ATCTCCAGCA GGACAGGGGG CAGATCCTGG
 TGGTCTGCTT GATAGGCCTC ATGGTGCTGT TCATCATTT AGTCATTGGC
 GTCTTGCACC TGCTGTACATC CTCTTCGGAA ACATCGAAA AAGAAGAAGG
 AAGAGAAAAT GGAAACTTTG AGTAAAGATA AAACCTCCAT AAGTGAAGAT
 ATTCAAGAGA CCAATATTGC TTAACTTAAT GATTATAAAG TTACCACAAG
 CTGATGGCGA GCTCCAAAAG ACCTGACTCA TTTGCAGATG GACAGGACAT
 GTCTCAGGAA AACAGCTTGC AGAAATGAAT GTTTAAATAT TGTATTTGCT
 TTTTCATTTT ATTTGTAACT GTGTGTTGTT ATTGTTTTA ATAATGATAT
 TTTTGTACCA GTCTGATAGC TGAGAAAAAA ATGACCTGGT TAGGTGACGA
 CAATAAGGGA CATTGAATAT AAACCTTGTG GCTAGGATTAA TAAACAAAC
 AAAATTGGA AAGAAGTTAG ATTTTAAGAA CTGAGTCATG GTCAGGCAGC
 GATGGCACAC ATCTTTAACATC CCAGCACTTG GGAGCAGAGG CAGGTAGATC
 TCTGGGAGTT TGAGGTCAAGC CTGGTCTACA AAGCAAGATC CAGGGTAGCC
 AAGGTTATAT AGAGAAACCC TGTCTCACAA AACCAAACCA ACCAATCAAC
 CAAACAGCAA AACACCTGAG TCGATAAAAG GGCTCCCCAG GTTTATACAC
 TTACCGTATG CTAAGAGCTT GAAATATATT GTTTCGTTT ATCGTTCACT
 AGTCTGTGAG ATTGCATTT TTCTCATTCC TATATATAAA AAAGTTAAAT
 GATTCCCTT AGATGTAGAG ATAGAGGAAG TTAGCGATGC CATAGCTTT

FIG. 36

PSGen 27-Novel

NTCNNTTNN CNNNGGCTGA TATCNGGCNC TTCNTCCNCG ATCNCAGATA
 CNNGNCACC GGNNNNTTCN GNNGTNATCN TCCNCCATCT CTCNTCCCCG
 ACNTGCACTC CGGGTNTNNT ACACNGGACA CTGTATCNNA CAGNAAACCT
 NCCNGGCC CAGGGATCAC CATNCCTCGN CCCNGCNTGT NTATAANATC
 AGNNNNTACA TCNANGAACN NACTATCACN GNTCTCTNTT NNCTCAGTGT
 NCACCTTCCA CTNCNGAACN TNNTCGCTNC NCCNCNGTTG GGAAAGGCAG
 NCNGTNCCGG CNACATGCCG TTTNCNCNT CTGNNCACNT GGGGATCTNC
 TNCAANGNAA TCAATTNGNG TAACCCACGG TTTNCNAAT CACTACTCT
 CANNCNANGG CCNTTGAANT GTTATCCCAC CACCANGGGG CNANTCGGA
 CCTNACAAATT CATCCTCAGC CGGCCCGAGN CTTAAAAAAAT TCAAAGGNCN
 CTTGCCCGCN TTNTTNCCCT AGCCCGCCNC CNGACAACAN CCNANNAACA
 ACCCCCCNNTC TTANGTGNCN NANCCACAG GANNTTGNNA TACCGGGTTT
 CCCCNNGAAAC TNCTCAANGC CNCCGTTCCA ACCCCCCGTTA CGAAACCGTN
 CCCNTTCCCT TCCGAGNTTG CCTATTAANN CCCCCNAAGT TCTNCTTCGT
 TNGNTTCCTC CGAAANG

- 1 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: The Trustees of Columbia University in the City of New York

(ii) TITLE OF INVENTION: RECIPROCAL SUBTRACTION DIFFERENTIAL
DISPLAY

10

(iii) NUMBER OF SEQUENCES: 24

(iv) CORRESPONDENCE ADDRESS:

15

- (A) ADDRESSEE: Cooper & Dunham LLP
- (B) STREET: 1185 Avenue of the Americas
- (C) CITY: New York
- (D) STATE: New York
- (E) COUNTRY: USA
- (F) ZIP: 10036

20

(v) COMPUTER READABLE FORM:

25

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

35

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: White, John P.
- (B) REGISTRATION NUMBER: 28,678
- (C) REFERENCE/DOCKET NUMBER: 55551-C-PCT/JPW/AKC

40

(2) INFORMATION FOR SEQ ID NO:1:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5	TAAANCGGTG GTACTGCTGC ACGGTCCCTCC GGGTACTGGA AAGACATCCC TTTGTAAGGC	60
	ATTAGCCAG AAACTGACCA TCAGACTGTC AANCAGGTAC CGGTATGGCC AGTTAATTGA	120
	AATAAACAGC CACAGCCTAT TTTCTAAGTG GTNTTCAGAA AGTGGCAAGT TGGTAACTAA	180
10	GATGTTCCAG AAGATTCAANG ACTTGATTGA TGATAANNAAC NCTTTGGTGT TTGTCCTGAT	240
	TGATGANGTA AGCACTCANN GGTACTCATT CTTNGTCTGC ATTGCCTCTT GCTATTACTG	300
15	CCTGATCCCT CTCATTTGGT TCACTGTGTC GCNANCTCTT TTCTATGGAT CTTTCCNAN	360
	CCACCCGTTT C	371

20 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- 25 (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5	GTGACGTAGG GTCTGTTGCG TCAATGGTTA TAGCAAGTGA TGCTCTCTGA TTATTACTGC	60
	TGACAATACT CGGCCAACAA TTCTTGCATA GAGTGCTGAT AAATAACTAT GTTACAAAAAA	120
35	GGGGTGGTCC CTGGAGAACAA TTACAGGCTT CCCTAGGTAA GTGTGCAGGT CAGGAGACGG	180
	CATATTCAAT CAGATGGCTG ATAGTTCTCC GTGGTTATGC ACCGGCTCCA GCTTGCCTAC	240
40	GTCAC	245

(2) INFORMATION FOR SEQ ID NO:3:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCAGCATGAT	GAATTTAATG	CAACAGTCAT	AGCAGGGCAA	GGGGAGAGAA	AGGCAGATGG	60
ACTATCTGCA	TCATCAAGCG	AGGGCTTGTG	TGGCGGGCTA	TGTGCAGAGA	CGAGCAGGGC	120
10	GAGGCACCTTA	AAAGCTGCTN	GATGAAAATC	CACCCAGGAG	AANTCTGGC	178
	CTACGTCA					

15 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGACGTAGGC	CCAGACTTCT	CCTGGGTGGA	TTTCATCCA	GCAGCTTTA	AGTGCCTCGC	60	
CCTGCTCGTC	TCTGCACATA	GCCGCCGACA	CAAGCCCTCG	CTTGATGATG	CAGATAGTCC	120	
30	ATCTGCCTTT	CTCTCCCCCTT	GCCCTGCTAT	GACTGTTGCA	TTAAATTCTAT	CATGCTGCCA	180
	AAAAAAAAAA A						191

35 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCCATAAATA	CACTTTATT	CATTGAAAT	GCATAATCAC	ACTGGGAGCA	CTCCCTTGG	60
AGCACTCCTC	TAGCAGCAGG	TCCGAAGTGC	TCCAGCATCG	TCAGCTGGCT	CCAACACCTA	120

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124

CGTC

(2) INFORMATION FOR SEQ ID NO:6:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTGGAAACA GAATAAGTG CTTTATTCCTC TGGCTGGCTC TCCTACGTCA

60

(2) INFORMATION FOR SEQ ID NO:7:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

30 TCGGGCGATAG CATTGGAGCA AGTCTTATCA GCAAGCAATG TTTTCAGTTA TGTTTCAAAG 60
TTAAGAAATGG GTTTAAACTT GCTGAACGTA AAGATTGACC CTCAAGTCAC TGTAGCTTTA 120
35 GTACTTGCTT ATTGTATTAG TTTANATGCT AGCACCGCAT GTGCTCTGCA TATTCTGGTT 180
TTATTTAAAAT AAAAAGTTGA ACTGCAAAAAA AAAAAAA 216

(2) INFORMATION FOR SEQ ID NO:8:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

4.1.1. MOLECULE TYPE: cDNA

- 5 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

	TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TNGCCAGGCT ATGTCTCAGA	60
5	CTTTATTATT ATTATTATTA TTATTATTAT TATAAATAAA ACATGTNCTT TCAATTAGGT	120
	TACAANAGTA TTTATCTCCA TAACGCTTCT TCATACATCC TTAGTTTGG ATTAAAGTAC	180
10	CATCCACCCC AACTCAAAC GTAAACCCCCA GTAATCCCCCT CTAACGTGGA AATTCTGGT	240
	TTAACAAACTC AGTTAACTGC CCCACAAACA GTGGGAGGCC GCTCTTGAT GGCTATGCCA	300
	CGTAACCCTT CACTGCTTCA CTTCTTCGCT GGCT	334

15 (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

	GACCGCTTGT ACCATCCAAC TTGCTTGTC TTCTGCAGAG AGGAGGCTAA AGCCCTTGAG	60
30	CTGGCTGGCA CTGTACTCAG GCCGGAAGCC CAGCTCGTCC CGGTTCTTGA CAAAGCAAGT	120
	TGGATGGTAC AAGCGG	136

(2) INFORMATION FOR SEQ ID NO:10:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

45	TGCCGAGCTG GGTATTGTGA CGGTTGATAA TGGCGGCATC ATGTTGCCAG GTACCGGGTA	60
	AGCAGACCTC AGAGCACAGC TTATTGTCCA GTGCTTTCAC GCTCGCGACG TCAAAGTCAT	120

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	TGTTATTGTC ACACCCATG CCTAGAAATG CGCATGTCCT CTGGCCATCT TCTTGCACAG	180
	GGGATCTGTC CTCTCCTCC ATGATATCAT TTCCCTCTGC ATCCTGCTCT CCAGCTGGAA	240
5	GGCCAGCAAA ATTGCTGTCT GGGGACTCTG CTGGGGTCTC CTCCCTTTCT GAAGGGGCC	300
	TGCTAGCAGC TCGGCA	316

(2) INFORMATION FOR SEQ ID NO:11:

10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: cDNA

20

AGGGGTCTTG ATGGACTTGG GTCGGACATC TTAGTGACCT GTGAATTCTT CTGTGGAGGC	60
TGAGTCTCAC GTAGCCGAGT TTAATATCTG TGCTATTAC TAAAGTATCT GCCACCAAAT	120
25 TGTACCAACT CATA GTTTTA TATGAATGTT GATGAGTCTG TATCATAAAT AGAATTGTTG	180
ATACATCCTT AATTG TGCA ATATTGTATG AAGAAGATTG TTATCAATTA AAACCACGCC	240
TCTTTATGAT CCTNNNAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	300
30 AACCNCCCTCA AATCCATNGG TTCTAACCCA AAACCT	337

(2) INFORMATION FOR SEQ ID NO:12:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

45

TTTTTTTTTT CATAACCCAT CAAACCAATT TTATTTCTAT AGCAACGTTT CTCACGTCTG	60
AACCTGAGAA TAAGTCACCA GCTCTTGACA GTAAACATGG GCCCTATCAA ATTATATTAG	120

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ACTCCTCAGT GTCCCGCCAT GTGGCCTTGC ACCAAATCAA TTAGTTGAG GGCCAAAATC	180
CTGTTGGGTT TCAAATAAAG TGTCAGGTCA TAAGGAGGGG GAGGGACTCA ATTCAATGGGA	240
5 ACATTTTAC CTGTTCAAAT AGATAAACTG AATTGCCCTA TCTGTGGTCA CCTGGATCCA	300
AGACCCT	307

(2) INFORMATION FOR SEQ ID NO:13:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

20 CCCTGACGAT AAATGGTAAG GAACTTTTTT TTTTTTTTTT TTTTTTTTT NC	60
GAAATAAACAA AACACAGCTT ATTATTTGGG GGAACATTAA NTTCTATAAN TGAACACAAA	120
25 ANAAAATTAA NANTTAATGG GGGGTANAA GGGACTTTGA ATCTATCTGG TATCATGACA	180
TTGAAGCANA NACCTGANTG ACCAGAAAGA GAGAGAGAGA GAGAGAGAGA GAGAGAGAGA	240
GAGAGGTTTC ATATGAGCTA GTGTTACAGG CTTTATTAGT CTATTAGTCA GGGACC	296

30 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AATCGGGCTG GATGGGTGTA TCCGGCACTG TTTCGTAGCG GCAGCAACTG GGTGCTTCTA	60
45 TCTGAAAGCG GGCTTCACAA AAAC TACTGC GCCACCCGAC TCGCTGCGGC ATCGCCCGGT	120
GGCGAGTACC GTATCGCCTT TCCTGGTGCA GAAGAAAGTGT TTACAGGAGG CGGTCATTAA	180

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	CCGCAATCTG ATTCTGTTTT TTATTCTCCC TGGCGGGTGA TCGCGATCGG CAGTTGAAA	240
	ACGATCGTTG AATCCACGCT CGGGAATGAT GTGGCTTCGC CGCCAACGCT TACTGACATT	300
5	TCATTTGTAC AGCCCGATT	319

(2) INFORMATION FOR SEQ ID NO:15:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 287 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

20	GCCGAGCTGT GTAAAACCAT CTATCCTCTG GCAGATCTAC TTGCCAGGCC ACTCCCAGGG	60
	GGGGTAGACC CTCTAAAGCT TGAGATTTAT CTTACAGATG AAGACTTCGA GTTTGCACTC	120
	GACATGACCA GAGATGAATT CAACGCACTG CCCACCTGGA AGCAAATGAA CCTGAAGAAA	180
25	GCGAAAGGCC TGTTCTGAGG GTGAGATGAC AGCCACAGAG AGGTCACTGC CACTAGACCA	240
	GAAAGTGGAT GGAGATATAT ATTTGGACTG GTGTTTTTT CTGTCAG	287

30 (2) INFORMATION FOR SEQ ID NO:16:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

	ATCGGGCTGC AGATTGGAGA CAAGATCATG CAGGTGAACG GCTGGGACAT GACCATGGTC	60
45	ACTCATGACC AGGCTCGGAA GCGGCTCACCC AACCGTTCGG AGGAAGTGGT CCGCCTGCTG	120
	GTGACTCGGC AGTCTCTGCA GAAGGCCGTA CAGCAGTCCA TGCTGTCATA GCTGTAGTCA	180

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	GCCTAGACTT CTGCCCACTG ACCTTTNGG GCACTGAGAA CACATCCACG CTCTGTCTGT	240
	ATCTAGTTCT GGCTTCTGCT GTGTGCTANG CCCCCAGCTCT GAGGAGTAAC AGCTGATCCC	300
5	AAAGGTCCAA GCCAACCTTC TTACCCCTCA GCCCCCANCC CGAT	344

(2) INFORMATION FOR SEQ ID NO:17:

10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 300 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: not relevant	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
20	TTTTTTTTTT TTTGGGCAAC TATGTATTAA TTGTGTTGG AAGGCAGAGT GAGGGAGGAG	60
	ACCCCGAGCAG GAAGAAGACT GGGTGCAGTC TAGAGTTCCCT AGTCAAGAGT AGGAAGGTTT	120
	CTGTTATACC CATCATAGAA CGAGAGAGGG GGCTCAATAG ATCATCCCCT TTGTCTCTCC	180
25	ACGGGGCTTC TTGAGCTTCT CAAAGTTCTT CAGGATGATG TCATATAACA CAGCATAAGC	240
	GTTACGGATC TCCATGACCA TCAGCCGGAT CTCCTGGTAT TCCGCCTCGT CCAGCTCGGC	300

30 (2) INFORMATION FOR SEQ ID NO:18:

	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 461 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: not relevant	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
	AANATCTGCT TAAAAGTTCT TTAATTGTA CCATTCTTC AAATAAAGAA TTTTGGTACA	60
45	AATTAAAGAA CTTTTAAGCA GATGTTTGG TGCAACTAAT AGAAAAGATA AAGGCAGCCT	120
	GACATGCATG CACTGCCTCA GTGACCAGTA AAGTCACATG NCCTTGGGAC GTCAGCTTAG	180

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NTTTATCACN GTGTCCCAGG GGTGCTTGTCA AAGAGATAT TCTGCCATGC CAGATTCAAGG 240
GGCTCCCATC TTGCGTAAGT TGGTCACGTG GTCACCCAGT TCTTTAATGG ATTTCACCTG 300
5 CTCATTCAAGG TAATGCGTCT CAATGAAGTC ACATAAGTGG GGATCATTCT TGTCAGTAGC 360
CAGTTTGTA AGTTCCAGTA GTGACTGATT CACACTCTT TCCAAGTGCA GTGCACACTC 420
CATTGCATTC AGCCCGCTCT CCCAGTCATC ACGGTACACNT A 461
10

(2) INFORMATION FOR SEQ ID NO:19:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear
- 20 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

25 TGACGTAGGG CCGAGAGCAA CAAGCACAGA ACTCCTTCTC CAGTTTCACC CTGATGAACT 60
TGAGGCACTC TTCTGCAC TG GGAGGGGCCA GCCTGGGGC CAGGCACATT GGACACCACC 120
TTCCCATGGA CTACAGCGTC AATGCCATTG CCTTCTATTG CTATACCTTC TAGGGGCTGC 180
30 CCCTCTTCCC ATTCAAGCCAA CACTGAGTGT TGGGAGATTT CTCTTTTTA AAAACACATG 240
AGAAAATAAA TGCACTTTAC TCCCTCCCCA AAAAAAAA 280

35 (2) INFORMATION FOR SEQ ID NO:20:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

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	GTAGGCAATA AAATGTTTC AGAGGTGCGA AAAAGCTTT GTTTCTTAA ACCATTCTTA	60
	GTCTCTGCCA CACTTGACAC TCCGTCAAAG TGAGAAGCGA ACTAAAGACC AACTGCGGTG	120
5	GAAAATATTA TGTTTATGTA ATAAAAAAAATCATGTAAC TGCAAAAAAA AAAAAAA	177

(2) INFORMATION FOR SEQ ID NO:21:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

20	TGCCGAGCTG AAAACATACA TCCGCACCGG GTTGAGATAG CTGGCCCTCC GTCCCCGGGC	60
	ATACTCTTG GATAAGAAC CCGGCCTTGT TACCAGGTAC CGGAGTGAGC TGAAAAATT	120
25	ACCGTCGAAA TGGGTGATGT CCTGGAAAAA ATGGTTCACC AGCTGCCAGG CAGATTCTTT	180
	GGGTTCCACA TTTTCCTGCC CACAGATGTG GCAGAAGCGG TCAAGTAATG CAGCATTACA	240
	ATTGAGGCAG ATCTTTCTT TTCTTCCTT GGAGTGGCTC AACCAAGCGAT TTTGGTTAAA	300
30	AATAATCAAA AAAGCGACGG CAAAACTTTT GTTATATTCC CGCCTGTGGC ATTTGAACTG	360
	TGCCCGGCAA CCGAATAACT TTTAATTTG AAAATAAAAT GCATACTAGA TTTTAGCGG	420
35	TTGCCTCCTG GCCATTGCTT CAGGCCCGNG CACAGCGTCA GCCCAGTTT ACCACNANGA	480
	ATATCCTAAG CGTTGAAACA GGGCACAGCC GAAAAAAACN CTGGCNACAA AAAANATCCG	540
	GACATCCTTT TTCCAATTTT GAAACCGAAN GCNCGAAAC NAAGGTTCTT CGGGAAAAAA	600
40	AATCGCCAAA ATACNCGANA TCAAACNTC CAA	633

45 (2) INFORMATION FOR SEQ ID NO:22:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

10	TGCCGAGCTG GGGGGAGTTC CAGGAATTG TGGACTATTT CCAGGAGGAA TTGAGGAATC	60
	TAGAAGTAAT AAGAACTTCA CAAGTAGAAC AACAGAGTTA ATTGACCTCT ATCCTTAAGA	120
	GTTACCAGAG AATTATTAAA AACTAAAGA ACAATCAAAG CCTGGTCCTG TGCCACCACC	180
15	CAAAAACATG TATAGCCTAT GTGCAGCTCG GCA	213

(2) INFORMATION FOR SEQ ID NO:23:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 679 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: not relevant
	(D) TOPOLOGY: linear
25	(ii) MOLECULE TYPE: cDNA

30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
	CTCANAGGGC NNNNTNGNGG NCNTCATGCN CCAGGNTCCN NCCCCANAN GANCNNCCNG	60
	GTAAACTACA CNGGAGTACT TAAGTGGACA NNCCACATGC GANGGNCAAG GGGATCACCN	120
35	TCNCTCCTNC AGNCTNTNCG TGNCTCTCCT GTNCNTNCAC TGCCNCANAA NGGANGCNCN	180
	NNCTCCTATC TGTNTACAGN AAACNTNGCN CTNNCTCTAA GCTCNCCCAC TNTGTGGAAA	240
	GGCNATGTGT GCGTGCCTCT CCCCTATCAC GGCGNGTTGC NAAANGGGGA TGTNCTGCNC	300
40	GGCGATGAAG TTNGGTCACT CCATGTTCC CAGTCCNACC TGTTAGACNA AGNATTGNAN	360
	TGTGATAACGA CTCNCTGTAA GGGGANTNGC GGACCCAGTA TGTTTGGCCC NACNNCCACT	420
45	TCTTTAAATG GTGGCTAACG GCGCTTCCTA GNATAAACAC TATTGGTCCC CCCCTCTGCA	480
	GNACCCNTTA CTTCCGNANA AAAATTGTTG TCNTGATCCG CGACAACCAC ACCGTCTGTN	540

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	GNTTTTAGTT GCAACNCNNA TCNCTCCAAA AAAGTTTCAG AAATCTTCAT TTTCCCNGGT	600
	TGAGGCCNTG ACAAAACCCCT NAGGATTGT CGAATGTAAA GTCTCCNGAT CTTCAATAAA	660
5	NNTCCAAAAG NCTANCGAT	679

(2) INFORMATION FOR SEQ ID NO:24:

10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 717 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: not relevant	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
20	NTCNNCTTNN CNNNGGCTGA TATCNGGCNC TTCNTCCNCG ATCNCAGATA CNNGCNCACC	60
	GGNNNTNTCN GNGGTNATCN TCCNCCATCT CTCNTCCCCG ACNTGCACTC CGGGTNTNNNT	120
25	ACACNGGACA CTGTATCNNA CAGNAAACCT NCCCNGGCC CAGGGATCAC CATNCCTCGN	180
	CCCNGCNTGT NTATAANATC AGGNNNNTACA TCNANGAACN NACTATCACN GNTCTCTNTT	240
	NNCTCAGTGT NCACCTTCCA CTNCNGAANC TNNTCGCTNC NCCNCNGTTG GGAAAGGCGA	300
30	NCNGTNCCGG CNACATGCCG TTTNCGNCT CTGNNCACNT GGGGATCTNC TNCAANGNAA	360
	TCAATTNGNG TAACCCACGG TTTNCNAAT CACTACTTCT CANNCNANGG CCNTTGAANT	420
35	GTTATCCCAC CACCANGGGG CNANTCGGGA CCTNACAATT CATCCTCAGC CGGCCCCAGN	480
	CTTAAAAAAAT TCAAAGGNCN CTTGCCCGCN TTNTTNCCCT AGCCCGCCNC CNGACAACAN	540
	CCNANNAACA ACCCCCCNNTC TTANGTTGCN NANCCCACAG GANNTTGNNA TACCGGGTTT	600
40	CCCCNGAAAC TNCTCAANGC CNCCGTTCCA ACCCCC GTTA CGAAACCGTN CCCNTTTCCCT	660
	TCCGAGNTTG CCTATTAANN CCCCCNAAGT TCTNCTTCGT TNGNTTCCTC CGAAANG	717

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/04323

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C12P 21/02; C12Q 1/68; C12N 15/11
US CL : 530/350; 536/23.1; 435/6

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/350; 536/23.1; 435/6

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
NONE

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
APS, MEDLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 4,981,783 A (AUGENLICHT) 01 January 1991, col. 2, lines 40-64.	19
A	US 5,599,672 A (LIANG et al.) 04 February 1997, see entire document.	1-40

Further documents are listed in the continuation of Box C.

See patent family annex.

* Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Z"	document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means		
P document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

02 JUNE 1999

Date of mailing of the international search report

15 JUN 1999

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
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INTERNATIONAL SEARCH REPORTInternational application No.
PCT/US99/04323**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: 20-40
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

The Computer Readable Form (CRF) of the Sequence Listing as filed does not comply with 37 CFR § 1.821-1.824.
As such, claims 20-40 could only be searched in part, by word searching.
3. Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

